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Sequence 31, Appl
Sequence 42, Appl
Sequence 5, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 10, S199920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Appl
Sequence 40, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 17, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 147, Appl
Sequence 147, Appl
Sequence 148, Appli
Sequence 148, Appli
Sequence 148, Appli
Sequence 148, Appli
Sequence 149, Appli
Sequence 149, Appli
Sequence 149, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Appl
Sequence 43, Appl
Sequence 143, App
                                                               8, 2004, 12:43:41; Search time 23 Seconds (without alignments) 22.446 Million cell updates/sec
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/cgm2_6/ptodata/2/iaa/5B.COMB.pep:*
/cgm2_6/ptodata/2/iaa/6A.COMB.pep:*
/cgm2_6/ptodata/2/iaa/B.COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS.COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-549-008-43
US-08-802-981-143
US-08-311-383-31
US-08-549-008-42
US-08-52-981-142
US-08-202-981-142
US-08-200-321-5
US-09-461-697-21
PCT-US95-03610-5
US-08-483-444A-21
US-08-476-134A-30
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US-08-311-383-35
US-08-92-008-40
US-08-02-981-1
US-08-374-983A-5
US-08-377-781A-17
US-08-221-0781-8
US-08-221-0781-8
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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US-08-189-331-149
US-08-189-331-150
                                                                                                                                                                                               389414 seqs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                           using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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56
1 CISVPLSVPC 10
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Query
Match Length DB
                                           OM protein - protein search,
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Maximum DB seq length: 10
                                                                   March
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                                                                                                               Title:
Perfect score:
                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                         Sequence:
                                                                                                                                                                                                Searched:
                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
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Sequence 147, App Sequence 148, App Sequence 149, App Sequence 150, App Sequence 150, App Sequence 19, App Sequence 18, App Sequence 186, App Sequence 126, App Sequence 126, App Sequence 126, App Sequence 13, Appl Seque		and Methods and Use	; s 0; Gaps 0;
23 41.1 8 2 US-08-471-068-147 23 41.1 8 2 US-08-471-068-148 23 41.1 8 2 US-08-471-068-149 23 41.1 8 2 US-08-471-068-150 23 41.1 8 4 US-09-171-068-150 23 41.1 8 4 US-09-187-370-6 23 41.1 9 4 US-09-187-370-2 23 41.1 10 4 US-09-187-370-2 22.5 40.2 9 3 US-08-891-271-4 22.5 40.2 9 3 US-08-891-271-4 22.5 40.2 9 3 US-08-993-402-13 22 39.3 7 2 US-08-933-402-13 22 39.3 7 2 US-08-933-402-13 22 39.3 7 2 US-08-532-818-13	ALIGNMENTS	WESULT 1 US-08-331-383-33 Sequence 33. Application US/08331383 Sequence 33. Application US/08331383 Sequence 33. Application US/08331383 GENERAL INCRMATION: APPLICANT: Komoriya, Akira APPLICANT: Komoriya, Akira APPLICANT: Komoriya, Akira APPLICANT: Compositions for the Detection of TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 56 CORRESPONDENCE ADDRESS: ADDRESSES: Townsend and Townsend Khourie and Crew STRRET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco CITY: San Francisco STARE: California COUNTRY: USA ZIP: 94105 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MB-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 COMPUTER: APPLICATION DATA: APPLICATION NUMBER: US/08/331,383 FILING DATE: 29-684 ATTORNEY/AGENT INRORMATION: NAME: Dow, Karen B. REGISTRATION NUMBER: 16865-1 TELEPHONE: 415-326-2400 TELEPHONE: 415-326-2400 TELEPHONE: 415-326-2400 TELEPHONE: 415-326-240 TELEPHONE: 415-326-2400 TELEPHONE: 415-326-320 TELEPHONE: 415-326-320 TELEPHONE: 415-326-320 TELEPHONE: 415-326-320 TELEPHONE: 415-326-320	/ Match 64.3%; Score 36; DB 1; Length 9; Local Similarity 50.0%; Pred. No. 3e+05; les 4; Conservative 4; Mismatches 0; Indels
		RESULT 198-08-7 Sequence of the parties of the part	Query M Best Lo Matches

P 4

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US-08-331-383-31

Sequence 31, Application US/08331383

Patent No. 5605809

PATENT NO. 5605809

APPLICANT: Komoriya, Akira

APPLICANT: Packard, Beverly S.

TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 56

CORRESPONDENE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 3; Length 9;
Pred. No. 3e+05;
4; Mismatches 0; Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 36,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECHONE: (415) 576-0200
TELECHONE: (415) 576-0300
TELECHONE: (415) 576-0300
TELECHONE: CHARACTERISTICS:
LENGTH: 9 amino acids
TELENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Townsend and Townsend Khourie and Crew
One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,383
FILING DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-00T-1994
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: DOW, KARTEN B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 1686:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.3%;
50.0%;
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Market Pl
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::|:|:|
2 AIPMSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                         US-08-549-008-43

Sequence 43, Application US/08549008

Fatent No. 57143-1404

Sequence 43, Application US/08549008

Patent No. 57143-1404

APPLICANT: Romoriya, Akira

APPLICANT: Backard, Beverly S.

TITLE OF INVENTION: Compositions for the Detection of TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof NUMBER OF SEQUENCES: 56

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STRET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 143, Application US/08802981
Patent No. 6037137N:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Romoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,008
FILING DATE: 27-OCT-1995
CLASSIPICATION: 435
PRIOR APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/331,383
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 01605-000110US
TELECOMMUTICATION NUMBER: 01605-000110US
TELECOMPUTICATION NUMBER: 01605-000110US
TELECOMPUTICATION NUMBER: 01605-000110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-549-008-43
                                                                                                                                                                                                                                                                                                                                                                          STATE: Californic
COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SVPLSVPC 10
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Best Local Similarity
Matches 4; Conserva
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2 AIPMSIPC 9
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ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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US-08-802-981-143
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US-08-802-981-142

| Sequence 142, Application US/08802981
| Pattent No. 6037137
| GENERAL INFORMATION:
| APPLICANT: Romoriya, Akira
| APPLICANT: Romoriya, Akira
| APPLICANT: Packard, Beverly S.
| TITLE OF INVENTION: Compositions for the Detection of Enzyme
| TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
| NUMBER OF SEQUENCES: 231
| NUMBER OF SEQUENCES: 231
| ADDRESSE: Townsend and Townsend and Crew LLP
| STREET: Two Embarcadero Center, Bighth Floor
| CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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; Sequence 5, Application US/08212190A
; Sequence 5, Application US/08212190A
; Patent No. 5652203
; GENERAL INFORMATION:
    APPLICANT: KOHN, Elise C.
    APPLICANT: LIOTTA, Lance A.
    APPLICANT: KIM, Young Sook
    TITLE OF INVENTION: USES THEREOF
    TITLE OF INVENTION: USES THEREOF
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew
    STREET: Steuart Street Tower, One Market Plaza
    CITY: San Francisco
    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: Galifornia
COUNTRY: USA
ZIP: 94111.384
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Packet in PC comparible
OPERATION SYSTEM: Pc-DoS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
SOFFWARE: Patentin Release #1.30
SOFFWARE: Patentin Relea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: /product= "Nle" US-08-802-981-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AIPXSIPC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                 ó
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                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                       58.9%; Score 33; DB 1; Length 9; 50.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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Pred. No. 3e+05;
3; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STAID.
COUNTRY: USA
ZIP. 94111-3934
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: PL-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION WINBER: US/08/549,008
FILING DATE: Z7-OCT-1995
FILING DATE: Z7-OCT-1995
                                                                                                                                                             /note= "Xaa is norleucine."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STRET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 08/331,383
FILING DATE: 28-0CT-1994
ATTORNEY AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 3.762
REFERENCE/DOCKET NUMBER: 01665-000110US
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 5
OTHER INFORMATION: /product= "Nle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42, Application US/08549008
Patent No. 5714342
GENERAL INFORMATION:
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Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                    4; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 9 amino acids
amino acid
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                                                                                             NAME/KEY: Region
LOCATION: one-of(5)
CTHER INFORMATION:
US-08-331-383-31
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserva
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2 AIPXSIPC 9
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2 AIPXSIPC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-549-008-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-549-008-42
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(415) 576-0300
TELBFAX:
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                                                                                                                                                                         US-08-900-321-5
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      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CORRALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,190A
FILING DATE: 14-MAR-1994
CLASSIFITATION: 435
ATTORNEY AGENT INFORMATION:
NAME: HULLEY, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0
TELEPHONE: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acide
TTELEPHONES: anino acide
TTELEPHONESS: aningle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Kohn, Elise C.
APPLICANT: Liotta, Lance A.
APPLICANT: Min, Young S.
TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
NUMBER OF SUGURNES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.6%; Score 25; DB 1; Length 10; 66.7%; Pred. No. 2.7e+02; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDLIW IYPE: Floppy disk
COMPUTER: IRW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,321
FILING DATE: 25-JUL-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco CONTYE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFRENCE/DOCKET NUMBER: 015280-204100US
TELECOMOJICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-900-321-5; Sequence 5, Application US/08900321; Patent No. 5981712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-212-190A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 PLSVPC 10
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APPLICANT: COGENY NEUROSCIENCE, Inc.
APPLICANT: COGENY NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Ratz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEPATH
FILE OF INVENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
44.6%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.6%; Score 25; DB 3; Length 10;
44.4%; Pred. No. 2.7e+02;
iive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICATION:
TITLE OF INVENTION: USES THERBOF
TITLE OF INVENTION: USES THERBOF
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: IEM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 14-WAR-1995
TILING DATE: 14-WAR-1995
CLASSIFICATION: DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 10 amino acids
                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CVMTHLSLP 10
                                                                                                                                        TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CISVPLSVP 9
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Best Local Similarity
Matches 4; Conserva
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Gaps

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WESULT 12
US-08-476-134A-30

1 Sequence 30, Application US/08476134A

1 Parent No. 623910

2 GREERL INCORMATION:

APPLICANT: EYAL, JACOBA

APPLICANT: EYAL, JACOBA

APPLICANT: HAMILTON, BRUCE K.

APPLICANT: HAMILTON, BRUCE K.

APPLICANT: HAMILTON, BRUCE F.

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: 1950-00-24

CURRENT FILING DATE: 1990-02-22

PRIOR APPLICATION NUMBER: 07/483,527

PRIOR FILING DATE: 1995-05-25

PRIOR FILING DATE: 1995-05-25

PRIOR FILING DATE: 1994-01-24

PRIOR FILING DATE: 1993-01

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTION NUMBER: 08/024,436

SEQ ID NO 30

LENGTRABLE
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.9%; Score 24; DB 1; Length 6; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%; Score 24; DB 3; Length 6; 100.0%; Pred. No. 3e+05; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BYAL, JACOB, HAMILTON, BRUCE K., TUSZYNASKI, GEORGE P.
TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF THROMBOSPONDIN FOR INHIBITING METASTASIS ACTIVITY NUMBER OF SEQUENCES: 32
                                    TELEPHONE: (215) 567-2020
TELEFAK: (215) 567-2991
TELEEX: 831-464
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                  TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 SVPC 10
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;Patent No. 5190920
                                                                                                                                                                                                                                                                                                                                    US-08-483-434A-21
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Sequence 21, Application US/08483434A

Sequence 21, Application US/08483434A

Sequence 21, Application US/08483434A

Settent No. 5648461

APPLICANT: EVAL, Jacob

APPLICANT: EVAL, Jacob

APPLICANT: TUSZYNSKI, George P.

TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and

TITLE OF INVENTION: Shithetic Analogs of Thrombospondin and

TITLE OF INVENTION: 346

CORRESPONDENCE ADDRESS:

REBET: 1601 Market Street, 36th Floor

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania

COMPUTER RADALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: DataHIL Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PLING DATE: DATALIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

PLING DATE: OLUMNIBE: US. 1914

PLING DATE: OLUMNIBE: US. 1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
44.6%; Score 25; DB 5; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-204000PC
REFERENCE/DOCKET NUMBER: 15280-204000PC
REFERENCE/DOCKET NUMBER: 15280-204000PC
REFERENCE/COCKET NUMBER: 15280-20400PC
TELEPHONE: (415) 543-500
ITELEPA: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36.317
REFERENCE/DOCKET NUMBER: 9598-3U6 (9049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: OS/UN 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/450,738
FILING DATE: 25-WAY-1995
RIOR APPLICATION NUMBER: US 08/185,614
FILING DATE: 24-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,436
FILING DATE: 01-WAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/587,197
FILING DATE: 24-SEP-1990
PRIOR APPLICATION NUMBER: US 07/587,197
PRIOR APPLICATION NUMBER: US 07/587,197
PRIOR APPLICATION NUMBER: US 07/587,527
                                                                                                                                                                                                                                                                                                                                                         amino acid
MEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-03610-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 PLSVPC 10
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Search completed: March 8, 2004, 12:47:08 Job time : 24 secs
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                                                                                                                                                                                                                                                                                                                              FEATURE
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APPLICANT: Recently S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STREET: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                            GEORGE P.
TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF
THROMEDSPONDIN FOR INHIBITING ANGIOGENESIS ACTIVITY
NUMBER OF SEQUENCES: 45
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,181
FILING DATE: 22-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                   42.9%; Score 24; DB 6; Length 6;
100.0%; Pred. No. 38+05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.9%; Score 24; DB 6; Length 6; 100.0%; Pred. No. 38+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5506208
PATENT: EVAL, JACOB, HAMILTON, BRUCE K., TUSZYNSKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION WHERE: US/08/331,383 FILING DATE: 28-0CT-1994
Sequence 35, Application US/08331383
Patent No. 5605809
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 131,565
FILING DATE: 04-0CT-1993
APPLICATION NUMBER: 895,764
FILING DATE: 09-UN-1992
APPLICATION NUMBER: 587,197
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.9
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                               4; Conservative
                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserva
                                                                                                                                                                                                                                       7 SVPC 10
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                                                                                      LENGTH: 6
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NAME/KEY: Region

LOCATION: one-of(8)

OTHER INFORMATION: /note= "Xaa is Pro or aminoisobutyric

US-08-331-383-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Region
LOCATION: one-of(5)
OTHER INFORMATION: /note= "Xaa is Met or norleucine."
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Dow, KATEN B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 16865
TELECHOMUNICATION INFORMATION:
TELEPHAK: 415-326-2400
INFORMATION FOR ENQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acids
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US-09-187-859-1374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1374, Ap Sequence 1374, Ap Sequence 1374, Ap Sequence 3970, Ap Sequence 1798, Ap Sequence 4046, Ap Sequence 2154, Ap Sequence 2154, Ap Sequence 2154, Ap Sequence 4040, Ap Sequence 4140, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Appl
Sequence 41, Appl
Sequence 1737, Appl
Sequence 1737, Appl
Sequence 2719, Appl
Sequence 2719, Appl
Sequence 24, Appl
Sequence 2747, Appl
Sequence 1885, Appl
                                                                           March 8, 2004, 12:36:04; Search time 23 Seconds (without alignments) 13.468 Million cell updates/sec
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6E_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-187-859-1374
US-09-187-859-1798
US-09-187-859-1798
US-09-187-859-3070
US-09-839-5428-1798
US-09-839-5428-1798
US-09-839-5428-1798
US-09-839-5428-1794
US-09-839-5428-154
US-09-839-5428-154
US-09-839-5428-154
US-09-839-5428-119
US-09-839-5428-1737
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                            389414 seqs, 51625971 residues
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                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 gummaries
                                                  OM protein - protein search, using sw model
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Match Length D
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Maximum DB seq length: 6
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28 20 52.6 4 1 US-08-548-540-120 Sequence 120, App 29 20 52.6 4 5 PCT-US96-09809-120 Sequence 120, App 31 20 52.6 5 4 US-09-322-791-4 Sequence 4, Appliance 20 52.6 5 4 US-09-322-791-4 Sequence 6, Appliance 20 52.6 5 4 US-09-394-630-13 Sequence 13, Appliance 20 52.6 5 4 US-09-394-630-13 Sequence 13, Appliance 20 52.6 6 4 US-09-819-542B-1591 Sequence 1591, Appliance 20 52.6 6 4 US-09-819-542B-1591 Sequence 1591, Appliance 20 52.6 6 4 US-09-819-542B-1591 Sequence 1591, Appliance 20 52.6 6 4 US-09-558-852-134 Sequence 1394, Appliance 20 52.6 6 4 US-09-558-852-134 Sequence 109, Appliance 20 52.6 6 4 US-09-558-852-134 Sequence 109, Appliance 20 52.6 6 4 US-09-558-862-1670 Sequence 109, Appliance 20 52.6 6 2 US-08-20-1464-4 Sequence 111, Appliance 20 52.6 6 2 US-08-20-1464-4 Sequence 111, Appliance 20 52.6 6 2 US-08-922-048-181 Sequence 111, Appliance 20 52.6 6 4 US-09-460-384-20 Sequence 21, Appliance 20 52.6 6 4 US-09-187-859-738 Sequence 23, Appliance 20 52.6 6 4 US-09-187-859-738 Sequence 23, Appliance 20 52.6 6 4 US-09-187-859-824 Sequence 824, Appliance 20 52.6 6 4 US-09-187-859-824
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AL I GNMENTS

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Sequence 1374, Application US/09187859A

Factor No. 618820D

FILE REPERBORE: 100086,4070I

FILLS PRIVARITON: COMPONIOS AND METHODS FOR MODULATING NONCLASSICAL

FILLS PRESENCE: 100086,4070I

MUMBERS C END NO. 4052

SOFTWARS: PatentIn Ver. 2.0

SEQ INNARIA: 1998-11-06

FRAUTH: 6

TYPE: FRT

OTHER INFORMATION: Cabherin: 7 cell adhesion recognition sequence

OTHER INFORMATION: Cabherin: 7 cell adhesion recognition

US-09-197-185-1374

A COMMENT OF SEQUENCE: 0; Mismatches 2; Indels 0; Gaps

OY 1 CVPLIC 6

DD 1 CEPKTC 6

DD 20-999-542B-1374

Sequence 1174. Application US/09839542B

RESULT 2

RESULT 2

RESULT 2

RESULT 3

RESULT 2

RESULT 3

RESULT 4: Symonds, James Matthew

A PAPLICANT'S Symonds,
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| Sequence 4046, Application US/09187859A
| Patent No. 6358920
| GENBEAL INFORMATION:
| APPLICANT: Blaschuk, Orest W.
| APPLICANT: Blaschuk, Orest W.
| APPLICANT: Gour, Barbara J.
| TITLE OF INVENTION: CADHENIN-MEDIATED FUNCTIONS
| TITLE OF INVENTION: CADHENIN-MEDIATED FUNCTIONS
| FILE REPERBACE: 100086.4071
| CURRENT FILING DATE: 1988-11-06
| NUMBER OF SEQ ID NOS: 4052
| SEQ ID NO 4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1799, Application US/09839542B
Fatent No. 656996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAMPONES NO.
TITLE OF INVENTION: CAMPONES NO.
FILE OF INVENTION: CAMPONES NO.
FILE OF INVENTION NOMBER: US/09/839,542B
NUMBER OF SEQ ID NOS: 4052
SOFTWARRE PATENTIN VET. 2.0
SEQ ID NO 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-09-187-859-4046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
THER INFORMATION: cadherin-12 cell adhesion recognition sequence
US-09-839-5428-1798
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66.7%; Pred. No. 3e+05;
rative 0; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserr
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Best Local Similarity
Matches 4; Conserv
                                                                   1 CDPKTC 6
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US-09-839-542B-3970
                                                                                                                                                                US-09-187-859-4046
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1999-11-06
NUMBER OF SEQ ID NOS: 4052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: GOUE, BADBARA J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-12 cell adhesion recognition sequence US-09-187-859-1798
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                    FEATURE:

OTHER INFORMATION: Representative cyclic modulating agent based on

OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
US-09-839-542B-1374
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                                                                                                                                    Query Match 68.4%; Score 26; DB 4; Length 6; Best Local Similarity 66.7%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.8%; Score 25; DB 4; Length 6; 66.7%; Pred. No. 3e+05; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3970, Application US/09187859A Patent No. 6358920
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1798, Application US/09187859A
Patent No. 6358920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
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SEQ ID NO 1798
                                                                                                                                                                                                                                      1 CVPLTC 6
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US-09-187-859-1798
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US-09-187-859-3970
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LENGIH: 6
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Sequence 2154, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 10086.4071
CURRENT APPLICATION NUMBER: US/09/187,859A
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Symonds, James Matthew

APPLICANT: Symonds, James Matthew

APPLICANT: GOUT. Barbara J.

TITLE OF INVENTION: COMPOUNDS AND WETHODS FOR WODULATING NONCLASSICAL

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

CURRENT APPLICATION NUMBER: US/09/839,542B

CURRENT PILING DATE: 2001-04-20

SOFTWARE: PATENTIN VOY: 4052

SOFTWARE: PATENTIN VOY: 2.0
                                                                                                                                                                                                                                                           OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Representative cyclic modulating agent based on "OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion of OTHER INFORMATION: recognition sequence US-09-839-542B-3573
                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 63.2%; Score 24; DB 4;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.2%; Score 24; DB 4; 50.0%; Pred. No. 3e+05;
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     FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SEQ TWARE: Patentin Ver. 2.0
SEQ ID 03573
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Sequence 3573, Application US/09839542B . Patent No. 6569996
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 3; Conserv
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1 CDPVSC 6
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1 CDPVSC 6
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US-09-187-859-2154
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                                                               APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPENS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION UNMER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3970
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-839-542B-4046

Sequence 4046, Application US/09839542B

Patent No. 656996

GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS

CURRENT APPLICATION NUMBER: US/09/839,542B

CURRENT APPLICATION NUMBER: US/09/839,542B

SOFTWARE: Patentin Ver: 2:0

SOFTWARE: Patentin Ver: 2:0
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APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Representative cyclic modulating agent based on CHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-09-839-542B-3970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Representative cyclic modulating agent based on CHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-09-839-542B-4046
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Sequence 3970, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7'
Matches 4; Conservative
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GENERAL INPORMATION:

GENERAL INPORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Synon, James Matthew

APPLICANT: Synon, Barbara J.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086, 407D1

CURRENT APPLICATION NUMBER: US/09/839,542B

SURRENT FILING DATE: 2001-04-20

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 4052

SOFTWARE: Refentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEMERAL INFORMATION:
APPLICANT: BROWN MICHAEL S.
APPLICANT: GOLDSFEIN, JOSEPH L.
APPLICANT: GOLDSFEIN, JOSEPH L.
APPLICANT: GOLDSFEIN, JOSEPH L.
APPLICANT: JAMES, GUY L.
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
TITLE OF INVENTION: TRANSFERASE INHIBITORS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSE:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
                                                                    2; Indels
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COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/429,964
FILING DATE: 27-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,625
FILING DATE: 16-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.5%; Score 23; DB 4; Best Local Similarity 66.7%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches
                   Score 23; DB 4;
Pred. No. 3e+05;
                                                                    0; Mismatches
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; Patent No. 6569996
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ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 66.77,
Thea 4; Conservative
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US-09-839-542B-4040
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US-08-429-964-41
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; Sequence 2154, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
    APPLICAMT: Blaschuk, Orest W.
    APPLICAMT: Symonds, James Mathew
; APPLICAMT: Symonds, James Mathew
; APPLICAMT: Gour, Barbara J.
    TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
    TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
; FILE REPERBNCE: 100086.4071
; CURRENT PILIAG DATE: 2001-04-20
; CURRENT PILIAG DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SEQ ID NO 2154
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS
CURRENT PALLING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4040
LENGTH: 6
                                                                                   FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-15 cell adhesion recognition sequence
US-9-187-859-2154
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O'THER INFORMATION: Representative cyclic modulating agent based on
O'THER INFORMATION: PB-cadherin cell adhesion recognition sequence
US-09-187-859-4040
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66.7%; Pred. No. 3e+05;
tive 0; Mismatches
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Patent No. 6358920
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ORGANISM: Artificial Sequence
                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
...t.hes 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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US-09-839-542B-2154
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                     LENGTH: 6
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CLASSIPICATION: 435

APPLICATION NUMBER: US 07/822,011

FILING DATE: ADANONED

CLASSIFICATION: 435

APPLICATION WHERE: PCT/US/91/02650

FILING DATE: 18-APR-1991

CLASSIPICATION: 435

APPLICATION NUMBER: US 07/615,715

FILING DATE: 20-NO/1990

CLASSIPICATION: 435

APPLICATION NUMBER: US 07/510,706

FILING DATE: DALEARE 1990 (ABANDONED)

CLASSIPICATION NUMBER: US 07/510,706

FILING DATE: 18-APR-1990 (ABANDONED)

CLASSIPICATION NUMBER: US 07/510,706

FILING DATE: 18-APR-1990 (ABANDONED)

TELEBRICE/DOCTET NUMBER: UTSD: 432/PAR

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION:

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 10
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	MHC H2-L antiqen -	glycogen phosphory		Ig heavy chain CRD	vitellogenin, 190k	T-cell receptor be	metallothionein-A	205K exoantigen -	polygalacturonase	T-cell receptor be	major postsynaptic	ATP-binding protei	cytochrome-c_oxida	hypothetical prote	R-phycoerythrin al	myomodulin - Calif	gene Cftr protein	stoma	collagen alpha 2(V	amicyanin - Paraco	sphingomyelinase -	protein P7 - curle	ä	alpha-gliadin 4Ha	alpha-qliadin 6Ha	Na+/K+-exchanging	flagellar protein	conopressin S - co	cytochrome-c oxida
SUMMARIES	ID	I65546	A60521	C39111	PT0247	A61622	PH0944	I51049	G33098	S62880	PH0926	A42689	B49712	S43630	E86128	B22565	A28340	157018	A60356	826508	A24407	C39745	D28027	865715	A61218	B61218	A32195	E42364	B28495	S77984
	DB	7	7	~	~1	7	N	7	N	N	7	7	~			~	7	7	~	7	~	~	~	~	7	7	~	~	~	7
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	간성	5.7	3.9	3.9	2.1	4.	4.0	9.6	3.6	9.6	9.6	8.	8.	8.	.8	0.0	0.0	25.0	0.0	0.0	0.	0.	0.0	5.0	0.0		5.0	3.2		3.5
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	Result No.		7	ю	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig heavy chain CRD hemagglutinin - in platelet activatin FC mu (IgM) recept phosphoprotein, bo dnaA protein - Pse alpha-1, 4-glucan-phypothetical colla tryptophyllin, bas seed protein we-5 aggrecan - bovine Ig H chain V-D-J r neural cell adhesi T-cell receptor be nitrate reductase enamelin f - bovin	ALIGNMENTS TESS146 MHC H2-L antigen - mouse (fragment) C;Species: Mus musculus (house mouse) C;Apecies: Mus musculus (house mouse) C;Accession: 16546 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P. C;Accession: 165546 A;Tile: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and the A;Reference number: 152778; MUD:86106202; PMID:3510743 A;Accession: 165546 A;Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234 Query Match 35.7%; Score 20; DB 2; Length 6;
PT0268 S51912 B4682 C3348 S11127 B34835 B34835 A35030 A41081 B61081 B61081 S45620 PH1602 PH1602 PH39690 PH3960 PH	ALIGNMEN TERSULT 1 165546 ANO Hab. Lantigen - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession 165546 R;Kimura, A.; Israel, A.; Le Bail, O.; Kouri Call 44, 261-27, 1986 A;Title: Detailed analysis of the mouse H-28 A;Title: Detailed analysis of the mouse H-28 A;Reference number: 152778; MUID:86106202; B,A,Cession: 165546 A;Koteule type: DnA A;Residues: 1-6 <res 20;<="" 35.7%;="" a;cross-references:="" gb:m12483;="" match="" nid:g199565;="" query="" score="" td=""></res>
000000004000000000	fragmenouse more_re ouse more_re Le Bai. of th MUID nslate 483; N:
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	RESULT 1 155546 MHC H2-L antigen - mouse (fragment) C;Species: Mus musculus (house mouse) C;Accession: 155546 R;Kimura, A.; Israel, A.; Le Bail, O. Cell 44, 261-272, 1986 A;Title: Detailed analysis of the mou A;Reference number: 152778; MUID:8610 A;Accession: 165546 A;Accession: 165546 A;Accession: 165546 A;Kstatus: preliminary; translated fro A;Molecule type: DNA A;Residues: 1-6 cRES A;Cross-references: GB:M12483; NID:91 Query Match 35.7%; Sco
~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	RESULT 1 165546 MHC H2-L anti C;Species: Mu C;Accession: R;Kimura, A.; Cill 44, 261- A;Tile: Deta A;Reference n A;Accession: A;Accession: A;Accession: A;Accession: A;Cross-refer A;Cross-refer A;Cross-refer

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Best Local Similarity 100.0%; Pred. No. 2.8e+05.
Matches 3; Conservative 0; Mismatches 0; Indels 8 VPC 10 셤 ð

Alternate names: glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
NyAlternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Sacession: A60521
Spanante, I.V.
Comp. Biochem. Physiol. B 95, 205-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal m
A;Reference number: A60521; MUD:90227907; PMID:2109669
A;Reference number: A60521; MUD:90227907; PMID:2109669
A;Reference number: A60521
A;Residues: 1-5 - BON>
C;Superfamily: glucan phosphorylase
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status exper

0; Indels h 33.9%; Score 19; DB 2; Length 5; Similarity 100.0%; Pred. No. 2.8e+05; 4; Conservative 0; Mismatches 0; Indels Query Match Best Local Similarity Matches 4; Conservat 2 ISVP 5 ð

2 ISVP 5

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C;Species: Rattus norvegicus (Norway rat)
C;Accession: PH094
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Richie: Analysis of T.cell receptor beta chains in Lewis rats with experimental aller A;Reference number: PH0891, MUD:92078857; PMID:1836012
A;Reference number: PH0891, MUD:92078857; PMID:1836012
A;Residues: 1-10 <GGL>
A;Residues: 
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C;Species: Oncorbynchus myKiss (rainbow trout)
C;Species: Oncorbynchus myKiss (rainbow trout)
C;Date: 13.58p-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: 151049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Bur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss)
A;Reference number: 151049; MUID:95324545; PMID:7601121
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C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
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R,Nichols, J.H.; Hager, L.P.
Rsubmitted to the Protein Sequence Database, May 1990
A;Recession: G33098
A;Accession: G33098
A;Accession: A33098
A;Accession: A3098
A;Recion: preliminary
A;Nichoule type: protein
A;Residues: 1-8 <NIC>
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Best Local Similarity
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C;Species: Lymantria dispar (gypsy moth)
C;Date: 21-01-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C;Accession: A61622
R;Hiremath, S; Eshita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A;Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantri
                                                                                                                                                                                C;Accession: C33111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simil A;Reference number: A39111; MUID:91156684; PMID:2000382
A;Accession: C39111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT02A7
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
B;Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:18999102
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                             C39111
Ig heavy chain C region - Pacific hagfish (fragment)
C.Species: Eptatretus stouti (Pacific hagfish)
C.Spate: 18-Oct_1991 #sequence_revision 18-Oct_1991 #text_change 16-Aug-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: protein
Residues: 1-10 •VAR-
C;Keywords: heterotetramer; immunoglobulin
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A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <HIR>
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ATP-Dinding protein p46 - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
C;Accession: B49712
R;Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
B;Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
A;Title: A set of endoplasmic reticulum proteins possessing properties of molecular chi
A;Reference number: A49712; MUID:94124514; PMID:8294423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiFreund, R.; Kadenbach, B.
Blochem. 221, Ill1-1116, 1994
Britle: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytoch: A;Reference number: 843624; MUID:94237150; PMID:8181469
A;Accession: 843630
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: E86128

C;Accession: E86128

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhr

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
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Pred. No. 1.1e+04;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <NIG>
C;Keywords: ATP; endoplasmic reticulum; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.8%; Score 15; DB 2; I
33.3%; Pred. No. 2.8e+05;
tive 1; Mismatches 3;
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A;Residues: 1-10 <FRE>
A;Note: the source is designated as Salmo gairdneri
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0, Mismatches
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Best Local Similarity 33.3
Matches 2; Conservative
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-10 <STO>
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                                         6 LSVP
                                                                                            2 LKVP
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C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH092 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
R;Gold, D.P.; Offiner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergiance number: PH0891; MUID:92078857; PMID:1836012
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                                                                                                                                                                                                  C;Species: Aspergillus sp.
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S62880
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C;5pocies: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 26-May-1994
C;Accession: A42689
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FEBS Lett. 382, 164-166, 1996
A;Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A;Reference number: S62880; MUID:96196586; PMID:8612742
A;Accession: S62880
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Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992
A;Title: On the identity of the major postsynaptic density protein.
A;Reference number: A42689; MUID:92212958; PMID:1313576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Experimental source: concanavalin A-activated lymphoblast A:Note: the authors translated the codon AGA for residue 4 as Thr C:Keywords: T-cell receptor
                                                                                                                                                                    polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.6%; Score 16; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 7.2e+03; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.6%; Score 16; DB 2; Length 10; 60.0%; Pred. No. 7.2e+03; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                            A,Molecule type: protein
A,Residues: 1-10 <STR>
C;Keywords: glycosidase; hydrolase
F;4/Active site: Tyr #status predicted
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Best Local Similarity 60.03
Matches 3; Conservative
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A; Molecule type: protein
A; Residues: 1-8 < WUA>
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A; Residues: 1-10 <GOL>
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2 VPLXL 6
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A;Cross-references: GB:AE005174; NID:g12519314; PIDN:AAG59489.1; GSPDB:GN00145; UWGP:Z59
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5903
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B-22565
R-phycocrythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: B22565
B;Glotz, A.V.; Glazer A.N.
J Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycocrythrin. A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Mccession: B22565
A;Molecule type: protein
A;Residues: 1-5 cMLO>
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                                                                                                                                                                                           0; Gaps
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                                                                                                                                    Query Match 26.8%; Score 15; DB 2; Length 10; Best Local Similarity 60.0%; Pred. No. 1.1e+04; Matches 3; Conservative 0; Mismatches 2; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                   141681 segs, 52070155 residues
                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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56
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                                                                                                                                   Title:
Perfect score:
Sequence:
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                                                                               Run on:
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Post-processing: Minimum Match 0% 'Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 10

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		iptio	P29177 bos taurus		_	P80331 oncorhynchu				P83455 pachymedusa		P82096 litoria rub		P80975 thunnus obe		P42984 leptinotars		fusa	P30087 homo sapien	penad	P80159 treponema h	_		P24047 stomogneute	•	P80336 oryctolagus		mytil	P13737 mytilus edu				periple	_	
SUMMARIES		qi	- ₽-	LPK2 LOCMI	COW2_CONPU	COXH ONCMY	NS1 MYCTU	TXL2 LOCMI						COXE_THUOB	COXQ_SHEEP	MNP1_LEPDE	ALL6_CYDPO	FUSS_FUSSO	UPA1_HUMAN	FAR5 PENMO	FLA2_TREHY	OXYT_BUFRE	RT33_BOVIN	SAP_STOVA	ANGT_CHICK	COXO_RABIT	UPA8 HUMAN	CIP1_MYTED	CIP2_MYTED	VP19_HSV1K	- 1	- 1			DNF1_LOCMI
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RESULT 2
LDRZ LOCMI

ID LDRZ LOCMI

AC PHENS COMI STANDARD; PRT; 10 AA.

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

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ascaris locuste squalus oryctolus oryctolus homo se homo se bothrous viperina oncorhy oncorhy	1.1.63) (6-0- eostomi; Bovoidea;	thylguanine-DNA stoichiometrically to a cysteine n: the enzyme is anine) + anine) + merryransFERASE	SIMILARITY).	0; Gaps
P43172 P41489 P42999 P32099 P30083 P30093 P31351 P31351 P31351 P80333 P80333	(EC 2.	bovine O6-methylguanine-DNA le in DNA by stoichiometricall O-6 position to a cysteine cide reaction: the enzyme is 6-O-methylguanine) + 6-O-methylguanine) + ADA AND OGT METHYLTRANSFERASE ESIDUES.	(BY	Length 9; ; Indels
S S S S S S S S S S S S S S S S S S S	T.1 BOVIN PRESENTANDARD; PRT; 9 AA. PROJIT; 01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) Methylated-DNAprotein-cysteine methyltransferase (methylated-DNA-protein-cysteine methyltransferase) Methylated-DNA methyltransferase) (Fragment). Bos taurus (Bovine). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec Rovidae; Bos. NORL TaxID=9913;	ine pos re retranet	ALKYL GROUP ACCEPTOR 325171A720476047 CRC64;	DB 1; 1.4e+05; ches 2
FAR9_ASCSU LIMT3_LOCMI OXYA_SQUAC OXYA_SQUAC OXYI_RABIT UPA3_HUMAN HPA3_HUMAN HPPB_PRUSE HPPB_POTIN BPP_TIPAS BRK_ONCMY COXK_ONCMY GS09_BACSU	T. 1 BOVIN MGMT BOVIN STANDARD; PRT; 9 AA. 101-DEC-1992 (Rel. 24, Last sequence update) 01-DEC-1992 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last sequence update) Methylated-DNAprotein-cysteine methyltransf methylguanine-DNA methyltransferase) (Fragmen MGMT) Bos taurus (Bovine). Bos taurus (Bovine). Bovinae, Butheria; Cetartiodactyla; Ruminants Bovidae, Bovinae; Bos. FULL TaxID=9913;	of gain at the second s	ALKYL GR 325171A720	Sco Pre 2;
	STANDARD; 1. 24, Created) 1. 24, Last sec. 1. 34, Last secprotein-cystei NA methyltransf ine). zoa; Chordata; ria; Cetartioda	UNE-Thymus; UB-Thymus; erg B., 014912; PubMed=2308822; erg B., 91411 J., Karran P.; ive site amino acid sequence (Putransferase.") eic Acids Res. 18:17-21(1990) FUNCTION: Repair of alkylated fransferring the alkyl group; ersidue in the enzyme. This is irreversibly inactivated. fordaring-the alkyl group; ersidue in the Schwigs of Sandaring-the Cont. [protain-L-cysteine = DNA (w. S-methyl-L-cysteine = DNA (w. S-methyl-transfc) FPC; FPCO(1974) Methyltransfc) FPC; FPCO(1974) Methyltransfc)	1 9 9 967 MW;	46.4%; 42.9%; vative 0
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4.0.8 C W W O U C W W W	BOVIN BOVIN S MGMT BOVIN S P29177; 01-DEC-1992 (Rel 01-DEC-1995 (Rel 01-DCT-1996 (Rel Methylated-DNA- methylat	Softer on	1 1 15	atc]
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mitochondrial electron transport.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome
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Submitted (DEC-1997) to Swiss-Prot.
-!- CAUTION: We are unable to find this protein in the translation of the genome of strain H37Rv.
NON_TER 1 1 1 1 1 1 NON_TER 1 1 1 SEQÜENCE 10 AA; 8767FE6AB2C73771 CRC64;
                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver;
MEDLINE-94237150, PubMed=8181469;
Freund R., Kadenbach B.;
Freund R., Kadenbach B.;
Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
Bur. J. Blochem. 221:1111-1116(1994).
In FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in
                                                                                                                                01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
Cytochrone coxidase polypeptide VIC (EC 1.9.3.1) (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.8%; Score 15; DB 1; Length 10; 75.0%; Pred. No. 4.5e+03; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c + 2 H(2)0.
--- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
PIR, S4530; S4530.
Oxidoreductase; Inner membrane; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA; 977 MW; E11B40769DC772DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15; DB 1; Ler
Pred. No. 4.5e+03;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
30 kDa non-secretory protein 1 (Fragment).
Mycobacterium tuberculosis.
                                                                                               10 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AA.
                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 26.83
Best Local Similarity 75.03
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.8
Best Local Similarity 37.5
Matches 3; Conservative
                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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1 MATPLVDP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ISVPLSVP 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=H37Rv;
                                                                                               COXH ONCMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NS1 MYCTU
P81135;
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SEQUENCE.
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                                                                           COXH ONCMY
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NS1 MYCTU
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                                                                                                                                                                                                                                                                                               Comp. Biochem. Physiol. 106C:103-109(1993).
-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Clipperton Island, TISSUE-Venom,
MEDLINE-99388839; PubMed=10461743;
Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                         "Isolation, identification and synthesis of locustapyrokinin II from Locusta migratoria, another member of the FXPRL-amide peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activity).

- SIMILARITY: Belongs to the pyrokinin family.

InterPro; IPRO01484; Pyrokinin.

PROSITE; PSO0539; PYROKININ; 1.

Neuropeptide; Amidation; Pyrokinin; Pyrrollidone carboxylic acid.

MOD RES 1 1 AMIDATION.

SEQÜENCE 10 AA, 1145 MW; CFAF421AA9D1B772 CRC64;
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0
Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Mollusca; Gaerropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                         Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J., de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19; DB 1; Length 10;
Pred. No. 8.8e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.1%; Score 18; DB 1; Length 8; 40.0%; Pred. No. 1.46+05; Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 4 D-LEUCINE.
8 AA; 890 MW; 75A367672732CEB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA.
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                                                                                                                                                                                      MEDLINE=94094539; PubMed=7903606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conus purpurascens (Purple cone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.9%;
57.1%;
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Matches 2; Conservative
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Best Local Similarity
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CVLLPP
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RESULT 3

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Length 10; Indels

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4 VPLSVP 9
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                   1 VXLSPP
                                                                               PACDA
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TRP7_LEUMA
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-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
-1- SIMILARITY: SOME SIMILARITY.
-1- SUBCUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Plasma protein map: an update by microsequencing.",
Electrophoresis 13:707-714(1992).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 4.4, its MW is: 49 kba.
SWISS-2DPAGE; P30089; HUMAN.
NON TER
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=90184489; PubMed=2311766;
MEDLINE=90184489; PubMed=2311766;
MEDLINE=90184489; PubMed=2311766;
"Locustatachykinin I and II, two novel insect neuropeptides with homology to peptides of the vertebrate tachykinin family.";
FEBS Lett. 261:397-401(1990).
                                                                                              Locusta migratoria (Migratory locust).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bopptera; Orthopteroidea; Orthoptera; Caellfera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
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01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 10) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93092937; PubMed-1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                  Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 1; Length 10;
Pred. No. 4.5e+03;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                  26.8%; Score 15; DB 1; Le 100.0%; Pred. No. 4.5e+03; iive 0; Mismatches 0;
                                                    01-APR-1990 (Rel. 14, Created)
1-APR-1990 (Rel. 14, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Locustatachykinin II (TK-II).
                                10 AA.
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4; Conservative
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                               STANDARD;
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
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                               LOCMI
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NON TER
SEQÜENCE
                                                                                                                                                                         SEQUENCE
                                         P16224;
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      RESULT 6
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smooth muscle.
-- SUBCELLULAR LOCATION: Secreted.
-- TISSUE SPECIFICITY: Skin.
-- TISSUE SPECIFICITY: Skin.
-- MASS SPECTROMETRY: MW=609.2; METHOD=MALDI.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
Amphibian defense peptide; Amidation, Hydroxylation.
MOD_RES 3 3 HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Myoactive peptide. Increases the amplitude and frequency of spontaneous contractions and tonus of hindgut muscle.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002) to Swiss-Prot.
-!- FUNCTION: Myoactive. Has selective relaxing activity on vascular
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Skin secretion;
Chen T.B., Orr D.F., Shaw C.;
"Pachymedusa dacnicolor tryptophyllin-1 (PdT-1): structural
characterization, pharmacological activity and cloning of precursor
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Phyllomedusinae; Pachymedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muren J.E., Naessel D.R.; "Seven tachykinin-related peptides isolated from the brain of the madeira cockroach; evidence for tissue-specific expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Eukaryota; Metazoa; Athhropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidaa; Dictyoptera; Blattaria; Blaberoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.0%; Score 14; DB 1; Length 7; 60.0%; Pred. No. 1.4e+05; rive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA; 794 MW; 7772D37DC7776350 CRC64;
                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Tryptophyllin-1 (Pdf-1).
Pachymedusa dacnicolor (Giant mexican leaf frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tachykinin-related peptide 7 (LemTRP 7).
7 A.A.
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MEDLINE=97269266; PubMed=9114447;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 60.v.,
Per 3; Conservative
STANDARD;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Cytochrome c oxidase polypeptide VIa (EC 1.9.3.1) (Fragment).
Thunnus obesus (Bigeye tuna).
Thunnus obesus (Rigeye tuna).
Robertory Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: 4 ferrocytochrome c + 0(2) = 4 ferricytochrome c + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in mitochondrial electron transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The subunit structure of cytochrome-c oxidase from tuna heart and
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Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
Kadenbach B.;
                                                      Gray W.R., Olivera B.M., Cruz L.J.,
"Peptide toxins from venomous Conus snails.",
Annu. Rev. Biochem. 57:665-700(1988).
-!- FUNCTION: Targets vasogressin-oxytocin related receptors.
                                                                                                                  -1- SUBCELLULAR LÖCATION: Secreted.
-1- TISSUE SPECIFICITY: Expressed by the venom duct.
-1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
-1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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SEQÜENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
                                                                                                                                                                                                                                                                                                  Score 13; DB 1; Le
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13; DB 1; I Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Inner membrane; Mitochondrion.
                                                                                                                                                                                                                                                                                      23.2%; Scur. No. 1...
100.0%; Pred. No. 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA.
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                                                                                                                                                                          InterPro; IPR000981; Neurhyp_horm.
Pfam; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
Biol. Chem. 262:15821-15824 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Biochem. 248:99-103(1997).
                                           MEDLINE=89024586; PubMed=3052286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.2%;
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.00
Thes 2; Conservative
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Best Local Similarity 60.0
Matches 3; Conservative
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                                                                                                                                                                                                                         Hormone; Amidation.
DISULFID 1
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SEQUENCE
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                             REVIEW.
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COXE THUOB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88058932; PubMed-3680228;
Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                          Litoria rubella (Desert tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms.";
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Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,

Apogastropoda; Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Neogastropoda, Conoidea, Conidae, Conus.
                                                                                                               Score 14; DB 1; Length 10;
Pred. No. 6.7e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.2%; Score 13; DB 1; Length 6; 66.7%; Pred. No. 1.4e+05; Live 1; Mismatches 0; Indels
                                                                    MOD RES 10 10 AMIDATION.
SEQUENCE 10 AA; 1068 MW; C4541679C9C865BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA; 792 MW; 6683704772C9A000 CRC64;
            -!- TISSUE SPECIFICITY: Brain.
-!- MASS SPECTROMETRY: MM-1069.7; METHOD=MALDI.
-!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
TACHYKININ, Neuropeptide; Amidation.
MOD RES. 10 10 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                               6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibjan defense peptide; Amidation.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                 25.0%;
75.0%;
                                                                                                                                              3; Conservative
                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                 Query Match
Best Local Similarity
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les 2; Conserv
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2 VPI 4
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EI01 LITRU
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Matches
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SSSS X E S
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Cýdia pomonella (Codling moth).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Drarricidae; Olethreutinae; Cydia.
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.4%; Score 12; DB 1; Length 8; 66.7%; Pred. No. 1.4e+05; ive 1; Mismatches 0; Indels
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8 AA; 936 MW; 0B2879C45B573767 CRC64;
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                                                                                                                                                                                                   30-MAY_2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
       Mismatches
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Job time : 11 secs
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Best Local Similarity 66.7
Matches 2; Conservative
     2; Conservative
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MOD RES 8
SEQUENCE 8 AA; 936 MW;
                                                                                                                                                                   STANDARD;
                                       5 PLS 7
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1 LPL 3
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                                                                                                                                                                                                                                                                                                                                                         Freund R., Kadenbach B.;
Submitted (MAR-1994) to Swiss-Prot.
--- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cypichrone c oxidase, the terminal oxidase in mitochondrial electron transport.
--- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 M(2)O.
---- SIMILARITY: Belongs to the cytochrome c oxidase VIII family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Head;
MEDLIABE=95380343; PubMed=7651886;
Spittabes K., Vankeerberghen A., Schoofs L., Torrekens S.,
Grauwels L., van Leuven P., de Loof A.;
"Identification, characterization, and immunological localization of
a novel myotropic neuropeptide in the Colorado potato beetle,
Leptinotarsa decemliant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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-!- FUNCTION: Myotropic peptide. Stimulates the contractions of the
                                                                                                                                                                                               (Fragment).

Ovis aries (Sheep).

Bukariota, Ketazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalis; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.
                                                                                                                     01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
Myotropic neuropeptide 1 (Led-MNP-1).
Leptinocarsa deceminata (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Chrysomelida;
Chrysomelini; Leptinotarsa.
Chrysomelini; Leptinotarsa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 13; DB 1; Length 10;
Pred. No. 1e+04;
0; Mismatches 3; Indels
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40.0%; Pred. No. 1e..
'~~ 0; Mismatches
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                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                               TISSUE=Heart, and Liver;
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Best Local Similarity
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COXQ SHEEP
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_phage:*
    sp_phage:*
    sp_plant:*
    sp_rodent:*
    sp_vertebrate:*
    sp_unclassified:*
    sp_vrirus:*
    sp_parcherias:*
    sp_parcher
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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Maximum Match 1008
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	035953 mis miscilli	O85598 moloney mir	085563 moloney mir	085619 moloney mir	056140 atreptococc	O7wuq2 escherichia	09v4x6 homo ganien	O7x6a3 zea maya sii	096041 cenothera h	O7v0i8 zea mays su	039957 hepatitis o	O15898 homo ganien	002831 orvetolams	O9trv3 ana an ina	ORTIGO ON TORNI	Q8ayl5 carassius a
SUMMARIES	DI	035953	085598	085563	085619	056140	Q7WUG2	Q9Y4X6	07X6A3	096041	Q7Y018	039957	015898	002831	O9TRY3	080VD3	QBAYLS
	DB	11	15	15	12	~	~	4	70	œ	10	12	4	ø	9	12	13
	Query Match Length DB	D	10	10	10	80	10	∞	6	10	10	10	80	8	80	σ	6
o)c	Query Match	35.7	35.7	35.7	35.7	33.9	33.9	30.4	30.4	30.4	30.4	30.4	28.6	28.6	28.6	28.6	28.6
	Score	20	20	20	20	19	19	17	17	17	17	17	16	16	16	16	16
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RESULT 2 Q85598

Q8aum7 carassius a Q8spn8 macaca mula	pyrrhob		⊣	Q8x4e5 escherichia	Q07624 rous sarcom	Q9x3k1 prochloroco	P72345 pseudomonas			antho	0		homod	dicra	Q8mbb7 merremia ae	Ø	P83091 spinacia ol	O90347 hepatitis q				E				
Q8AUM7 Q8SPN8	Q85AZ9	042564	Q9L5W6	Q8X4E5	207624	Q9X3K1	P72345	Q9K4M6	Q9UCSB	Q9TWV0	Q9FXL0	Q9H3R9	Q9H121	Q8MAZ9	Q8MBB7	Q8SL54	P83091	090347	Q8JV78	Q9PRU1	067113	Q8KPX4	049534	032560	QRIUBS	QBWFR5
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16	16	15	15	12	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	13	13	13	13	13	13
17	19	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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035953

AC 035953

BY TELIMINARY; PRT; 9 AA.

CO 035953;

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-OAT-2003 (TrEMBLrel. 05, Last sequence update)

DT 01-OAT-2003 (TrEMBLrel. 05, Last sequence update)

DE Truncated voltage-gated sodium channel alpha subunit (Fragment).

SCNBA.

SCNBA.

SCNBA.

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

NEB EQUENCE RROW N.A.

RP SEQUENCE RROW N.A.

RP SEQUENCE RROW N.A.

RP SEQUENCE RROW N.A.

RA Plummer N.W., MCBURINGY N.M.; Meisler M.H.;

RY Alternative splicing of the sodium channel SCNBA predicts a truncated RT "Alternative splicing of the sodium channel SCNBA predicts a truncated RT "Alternative splicing of the sodium channel SCNBA predicts a truncated RT "Alternative splicing of the sodium channel Chem. 272-24080-24015 [1997].

DR MGD; MG1:103169; ScnBa.

DR MGD; MG1:103169; ScnBa.

RWD; MG1:103169; ScnBa.

CONDICER:

RWD IN TER SEQUENCE 9 AA; 898 MW; 22D92865B735B737 CRC64;

COURTY MATCH 35.7%; Score 20; DB 11; Length 9;

Best Local Similarity 80.0%; Pred. No. 1e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps

A VPLSU S
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STRAINS-STI1;
MEDLINE-95047254; PubMed=7958782;
MEDLINE-95047254; PubMed=7958782;
MEDLINE-95047254; PubMed=7958782;
Constable A., Mollet B.;
"Isolation and characterisation of promoter regions from Streptococcus thermophilus.";
thermophilus.";
EMSEN Microbiol. Lett. 122:85-90 (1994).
EMBL; X78210; CAA55045.1;
NON_TER
                                                                                                                                                                                                                                                     Donoghue D.J., Hunter T.;

"Recombination junctions of variants of Moloney murine sarcom virus:
Recombination junctions of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).
J. Virol. 45:607-617(1983).
NON TER
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Moloney murine sarcoma virus (Strain m1) env/mos 5' junction (Fragmant).
Moloney murine leukemia virus.
Viruses, Retroid viruses; Retroviridae, Gammaretrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       35.7%; Score 20; DB 15; Length 10; 75.0%; Pred. No. 3.8e+03; tive 0; Mismatches 1; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=83164305; PubMed=6300424;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 75.0%;
Conservative
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Plasmid p541.
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Donoghue B.J., Hunter T.

Tecombination junctions of variants of Moloney murine sarcom virus:

Generation and divergence of a mammalian transforming gene.";

J. Virol. 45:607-617(1983).

EMBL; K03106; AAA46492.1; -.

NON TER

10 AA, 1081 MW; 7BECFCBEA771B5A4 CRC64;
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"Recombination junctions of variants of Moloney murine sarcom virus:
Generation and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).

BMBL; K03105; AAA46491.1; -.

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Moloney murine sarcoma virus (Strain HT1) env/mos 5' junction
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                                                                                                                                                     Moloney murine leukemia virus.
Viruses, Retroid viruses; Retroviridae; Gammaretrovirus.
NCBL_TaxID=11801;
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Best Local Similarity 75.0
Matches 3; Conservative
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SEQUENCE FROM N.A.
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GO, GO:0005739, C:mitochondrion; IEA. Mitochondrion; Ubiquinone.
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Mol. Gen. Genet. 240:445-449(1993).
EMBL; X69553; CAA49285.1; -.
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Schuster W.;
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Best Local Similarity 100.0
Matches 3; Conservative
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SEQUENCE FROM N.A.
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Matches
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                                                            Miriagou V., Tzouvelekis L.S., Villa L., Lebessi E., Vatopoulos A.C., Carattoli A., Tzelepi E.;
"Antibiotic Resistance Region of an IncN Plasmid Carrying an Integron-Located blaVIM-1-Metallo-b-Lactamase Gene and a Novel CMY-Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20108806; PubMed=10640831;
Drechisler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S., Schroth A., Bodem J., Royer-Pokora B., "Genomic structure, alternative transcripts and chromosome location of the human LIM domain binding protein gene LDB1.";
EMBL; AJ434309; CAB44408.1;
NON_TER
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                       1 33.9%; Score 19; DB 2; Length 10; Similarity 57.1%; Pred. No. 5.8e+03; 4; Conservative 1; Mismatches 2; Indels
                                                                                                                            Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY339625; AAQ16673.1; -
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                                                                                                                                                                  10 10
10 AA; 991 MW; 882D57A5B045A2D5 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Nuclear LIM interactor (Fragment).
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                 Cephalosporinase Gene.";
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Best Local Similarity
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                                                   SEQUENCE FROM N.A.
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1 MSVGC 5
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SEQUENCE
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Best Local Si
                                                                                                                                                       Plasmid.
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Mitochondrion.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Onagraceae; Oenothera.
                                                                                                                                                                                                                                                                                                            Gaps
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STRAIN-cv. 38-11, and cv. A632; Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M., Buckler E.S. IV.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
NCBL_TaxID=4578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Ribosomal protein gene rpl5 is cotranscribed with the nad3 gene
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Pred. No. 1.4e+04;
                                                                   "Dissection of maize starch production by candidate gene association.";
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                                                                                                            Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AY290305; AAR45331.1; -.
EMBL; AY290311; AAR45337.1; -.
NON TER.
9 AA; 976 MW; DF9BCEA76736C6DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ©96041;
01-FEB-1997 (TrEMBirel. 02, Created)
01-FEB-1997 (TrEMBirel. 02, Last sequence update)
01-MN-2003 (TrEMBirel. 24, Last annotation update)
NADH-ubiquinone oxidoreductase subunit 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA; 1097 MW; 723067B0476DD9CB CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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/ 100.0%; Pred. No. 1...
'... 0; Mismatches
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MEDLINE=92049376; PubWed=1719383;
Shimasaki S., Gao L., Shimonaka M., Ling N.;
"Isolation and molecular cloning of insulin-like growth factor-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Evidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";
Marrix Biol. 15:39-47(1996).
EMBL; 883371; AAD14433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBL_TaxID=9826,
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last amnotation update)
Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96377339; PubMed=8783186;
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
"Isolation of chromosome-specific genes by reciprocal probing arrayed cDNAs and cosmid libraries.";

Hum. Mol. Genet. 0:0-0(1995).

EMBL; L32078; AAA73888.1; -.

NON_TER 1 1

NON_TER 8

SEQÜENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;
                                                                                                                               28.6%; Score 16; DB 4; Length 8; 60.0%; Pred. No. 1e+06; ative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.6%; Score 16; DB 6; Length 8; 100.0%; Pred. No. 1e+06; ttive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                 01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-2003 (TrEMBLrel. 24, Last annotation update)
01-JUL-2012 (TrEMBLrel. 24, Last annotation update)
01-JUL-2012 (TremBlague Cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 1 8 AA; 1028 MW; B859C7272EA77371 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0
                                                                                                                              Query Match
Best Local Similarity 60.0°
Matches 3, Conservative
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SEQUENCE FROM N.A.
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MEDLINE=97366412; PubMed-9252602;
Smith D.B., Cuceanu W., Davidgon F., Jarvis L.M., Mokili J.L.,
Hamid S., Ludlam C.A., Simmonds P.;
"Discrimination of hepatitis G virus/GBV-C geographical variants by
analysis of the S' non-coding region.";
J. Gen. Virol. 78:1533-1542(1997).
BMBL, APRO3175; AACS7986.1;
SEMBL, ARO3175; AACS7986.1;
SEQÜENCE 10 AA, 1067 MW; CC88FE2727273772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Placenta;
Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,
Caskey C.T.H.;
                                                                                                                                                                                                                                                                                                                                                                     01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last amnotation update)
El protein (Fragment).
Hepatitis GB virus C.
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
GBV-C/HGV group.
NCBI_TAXID=39839;
                                     STRAIN-cv. KI44;
Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M.,
Buckler E.S. IV.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCEI_TaxID=9606;
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                                                                                  "Dissection of maize starch production by candidate gene association.";
                                                                                                             Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY290360; AAP45386.1; -.
NON_TER 10 10
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Q1-NOV-1996 (TrEMBirel. 01, Created)
01-NOV-1996 (TrEMBirel. 01, Last sequence update)
01-NOV-1996 (TrEMBirel. 19, Last annotation update)
(Clone XP6A11B) (Fragment).
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5 LPC 7
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MEDLINE=21580659; PubWed=11724134;
MEDLINE=21580659; PubWed=11724134;
Mine ovine respiratory syncytial virus F gene sequence and its diagnostic application."; and syncytial virus F gene sequence and its diagnostic application."; 455-461(2001).

EMBL, AF334398; AAL91343.1; -.

NON TER
SEQUENCE 9 AA; 1154 MW; 8B6A3EA764541415 CRC64;
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28.6%; Score 16; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels
Query Match 28.6%; Score 16; DB 6; Length 8; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                    Ovine respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyaoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=28869;
                                                                                                                                                                                Q8QVD3 PRELIMINARY, PRT; 9 AA. Q8QVD3; 01-UN-2002 (TEEMBLrel. 21, Created) 01-UN-2002 (TEEMBLrel. 21, Last sequence update) 01-UN-2002 (TEEMBLrel. 21, Last annotation update) Matrix protein 2 (Fragment).
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March 8, 2004, 12:39:00; Search time 52 Seconds (without alignments) 54.336 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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56
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geneseqp2003aa:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 29Jan04:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp20028:* geneseqp1980s:* Database

Maximum Match 100% Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aau04532 VEGF base	Aau04533 VEGF base	Aar96138 Protease	_	Aaw46562 Peptide b	Aar96137 Protease	Aaw82094 D-NorFES-	Aaw46561 Peptide b		Abu60357 D-NorFES-	Aau00643 Human mem	Adb88786 Membrane	Aau94301 Human nov	Aau94201 Human nov	Aau94811 Human nov	Aau94577 Human nov	Aam50003 Human D40	Aau95231 Human nov	Aau94696 Human nov		Aaq73418 Human qen	Sacche	_	Abr19062 Human can	Human
SUMMARIES	qi	AAU04532	AAU04533	AAR96138	AAW82212	AAW46562	AAR96137	AAW82094	AAW46561	AAG73245	ABU60357	AAU00643	ADB88786	AAU94301	AAU94201	AAU94811	AAU94577	AAM50003	AAU95231	AAU94696	AAU95023	AAG73418	AAG85638	ABG64264	ABR19062	ABR19524
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o40	Match	100.0	74.1	64.3	64.3	64.3	58.9	58.9	58.9	58.9	58.9	57.1	57.1	56.2	56.2	56.2	56.2	55.4	53.6	53.6	53.6				50.0	20.0
	Score	26	41.5	36	36	36	33	33	33	33	33	32	m	31.5	31.5	31.5	31.5	31	30	30	30	29	29	29	28	28
1,000	No	⊣	7	e	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	61	20	21	22	23	24	25

Abr18877 Human can Aar74541 Protease Adc71008 HLA motif Adc706887 HLA motif Adc70636 HLA motif Adc70653 HLA motif Adc70653 HLA motif Adc70653 HLA motif Adc70654 HLA motif Adc70658 HLA motif Adc7102 HLA motif Adc7104 Stan edit Adc7105 HLA motif Ad	SH3 Huma Huma Huma
6 ABR18877 2 AAR74541 7 ADC71003 7 ADC70887 7 ADC70359 7 ADC70732 7 ADC70732 1 AAR82104 9 ABG34945 5 ABG34945 5 ABG34945 5 ABG34945 5 ABG34945 6 ABG36540	4 AAC9603 4 AAC9603 4 AAE05003 4 AAE05003
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ALIGNMENTS

Human, VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; peoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. Location/Qualifiers 1. .10 /note= "This bond cyclises the peptide" Ą. VEGF based monocyclic peptide 10. AAU04532 standard; peptide; 10 (first entry) Key Disulfide-bond WO200152875-A1 26-SEP-2001 Synthetic. AAU04532;

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533 26-JUL-2001.

Cendron A; Stacker S, (LUDW-) LUDWIG INST CANCER RES. Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothellal growth factor). The invention relates to a method of producing a mnoneric monocyclic peptide by a measuring betabet a carbon separation distances on opposite antiparallel strands of a

Claim 49; Page 32; 102pp; English.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides (Comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis, contains a mammall with a condition characterised by anglogenesis, in a mammall with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, recondition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenois, head, heat or cold trauma, substance-induced neovascular sequelas, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF, VBGF-C or -D and care also used in combination with an anti-inflammatory agent, to treat a discuss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; pecrisats; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; ohronic inflammation; oyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 56; DB 4; Length 10; 100.0%; Pred. No. 0.0098; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF based monocyclic peptide 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU04533 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200152875-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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Matches
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The Bequence represents a monomeric monocyclic period by a measuring beta-
whose 3-dimensional structure is modelled on the expose loop of human

WRGFD (vascular endothelial growth factor). The invention relates to a
method of producing a monomeric monocyclic peptide by a measuring beta-
beta carbon separation distances on opposite antiparallel strands of a
cyclising the peptide by oxidising the cysteine residues. The monocyclic
peptides) and a cyclic peptides (comprising 2 linked monocyclic
peptides) and a cyclic peptide with at least one amino acid deleted prior
cyclisation are used to interfere with angiogenesis,
neovascularisation or lymphangiogenesis in a mammal with a condition
characterised by angiogenesis, neovascularisation or lymphangiogenesis.
The condition is diabetic retinopathy, psoriasis, arthropathy,
hemangioma, vascularised malignant or benign tumour, post-recovery
cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
trauma, substance-induced neovascularisation of the liver, excessive
corebrovascular accident, post-angioplasty restenosis, head, heat or cold
trauma, substance-induced neovascularisation of the liver, excessive
creption. The peptides are also used to modulate vascular permeability
cor brain. The peptides are used to image blood vessels and lymphatic
cor brain. The peptides are used to image blood vessels and lymphatic
cor brain. The peptides are used to image blood vessels and lymphatic
cor brain. The peptides are used to image blood vessels and lymphatic
cormulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
corbination in peripheral limbs or in lungs, peritoneal cavity, pleura,
corpusation and biological activity induced by VBGF. Or -D and
are also used in combination with an anti-inflammatory agent, to treat a
corpusation and accident and provine and accident an
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    .3
/label= C1
    /note= "the two conformation determining regions C1 and C2 which flank the protease recognition site peptide P are provided to position the two fluorophores within 100

                                                                                        The sequence represents a monomeric monocyclic peptide of the invention,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "labelled by donor fluorophore (F1) 5'-
carboxytetramethylrhodamine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protease substrate peptide with fluorophore at each terminus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.1%; Score 41.5; DB 4; Length 9; 90.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               angstroms of each other"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy
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18-DEC-1996
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Region
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Sequence 9 AA;
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                      20-FEB-1998;
                                            20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-OCT-1994;
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  27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Packard BS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW46562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                임
                                                                                                                                                                                                                                                                                                                              The present sequence is a specific example of a fluorogenic substrate for detecting activity of a protease. The substrate agrees with the generic formula (S1)n-C1(F1)-E-C2(F2)-(S2)k in which a peptide P of 2-8 amino acids comprising a recognition site for the protease is flanked by conformation determining regions (C1 and C2) of 1-3 amino acids. C1 and C2 are labelled by fluorophore groups (F1 and F2, respectively) positioned within 100 angstroms of each other. Additional peptide spacers of 1-50 amino acids (S1 and S2) may also be present (i.e. n and k = 0 or 1). Fluorogenic substrates corresponding to the generic formula are used to detect or localise proteases in biological specimens, esp. in frozen tissue sections or to monitor protease activity in stored reagents. Changes in protease activity are associated with e.g. arthritis, camplysem, thrombosis and cancer metastasis. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
//abel= C2
//abel= C2
//note= "the two conformation determining regions C1 and
C2 which flank the protease recognition site peptide P
are provided to position the two fluorophores within 100
angstroms of each other"
                                                                 /note= "labelled by acceptor fluorophore F2 rhodamine {\tt X} acetamide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease activity; fluorphore; detection; fluorogenic; cellular uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                               New fluorogenic peptide(s) with fluorophore at each terminus - for detecting protease(s) in biological samples, emit intense visible fluorescence when cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 9;
Pred. No. 1.4e+06;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-NorFES-A protease inhibitor peptide #2.
                                                                                                                                                                                                                                                                                                             Claim 16; Page 31; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW82212 standard; peptide; 9 AA.
                                                                                                                                                                          94US-00331383.
                                                                                                                                                    95WO-US013936.
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50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                       Komoriya A, Packard BS;
                                                                                                                                                                                                 ONCO-) ONCOIMMUNIN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conformation change.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      emphysema, thromb
correct PA field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
                                                               Modified-site
                                                                                                                                                                          28-OCT-1994;
                                                                                                                                                      27-OCT-1995;
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                                                                                                           WO9613607-A1
                                                                                                                                 09-MAY-1996.
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Region
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composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, polyacaccharides, proteins, peptides, lipids, phopholipids, glycolipids, glycoproteins, steroids or polymers. In addition, attachment of a hydrophobic group to amolecule can be used to enhance uptake by cells. The composition is composed of P = peptide comprising a protease binding site for the protease, Fl, F2 peptides = fluorophores where Fl is attached to the amino terminal amino acid and F2 is attached to the carboxyl terminal amino acid and S1, S2 peptides = when present, are peptide spacers where S1, when present, is attached to the amino terminal acid, and S2, when present, is attached to the carboxyl terminal acid, and S2, when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease binding site; protease; protease indicator; fluorescent signal; detection; protease activity.
                                                                                                                                                                                                                                                                                                                                                                   New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW82023-W82240 are peptides used in the construction of a fluorogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fluorogenic substrates for protease determination - having two closely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.3%; Score 36; DB 2; Length 9; 50.0%; Pred. No. 1.4e+06; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide backbone of a protease indicator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 52; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW46562 standard; peptide; 9 AA.
98WO-US003000
                                                                      97US-00802981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0054900B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-00331383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Komoriya A;
                                                                                                                                                                                                                   Komoriya A, Packard BS;
                                                                                                                                            (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                 WPI; 1998-467579/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-158345/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|:|:|
2 AIPMSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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acetamide"

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW82094
   ⋩
                                                     The present peptide contains a protease binding site. It is used to produce novel reagents whose fluorescence increases in the presence of particular proteases. These fluorescence indicators (substrates) produce novel reages. These fluorescent signal at a visible wavelength when they are digested by a protease. The fluoregenic indicators have the centaining a protease binding site e.g. AAW4650-53, AAW4656. Fr and F2 containing a protease binding site e.g. AAW4650-53, AAW4656. Fr and F2 containing a protease binding site e.g. AAW4650-53, AAW4656-Fr and F2 containing a protease binding site e.g. AAW4650-53, AAW4656-Fr and F2 containing a protease binding site e.g. AAW4650-53, AAW4654-58. n. k = 0 or 1. Cl and C2 are conformation-determining regions that introduce a bend into the composition which positions the fluorophores adjacent to cach other with a separation of less than 100 Augstrom. When n is 1, S1 is joined to the terminal carboxy group of Cl by a peptide bond, and when k is 1, S2 is joined to the terminal carboxy group of C2 by a peptide bond. The protease indicators are used for detecting protease activity in a biological sample. The sample is contacted with the indicator and any change in fluorescence is detected, an increase in
                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //Jabel= C2
//Jabel= C2
//note= "the two conformation determining regions C1 and C2 which flank the protease recognition site peptide P are provided to position the two fluorophores within 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "the two conformation determining regions C1 and C2 which flank the protease recognition site peptide P are provided to position the two fluorophores within 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "peptide comprising a protease recognition site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "labelled by acceptor fluorophore F2 rhodamine X
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fluorogenic substrate; fluorophore; protease activity; assay; visible fluorescence; in situ detection; frozen tissue section; histology; arthritis; emphysema; thrombosis; cancer metastasis.
                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "labelled by donor fluorophore (F1) 5'
carboxytetramethylrhodamine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protease substrate peptide with fluorophore at each terminus.
                                                                                                                                                                                                                                                                                                                                                          64.3%; Score 36; DB 2; Length 9; 50.0%; Pred. No. 1.4e+06; ive 4; Mismatches 0; Indels
spaced fluorophores flanking protease binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angstroms of each other"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angstroms of each other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR96137 standard; peptide; 9 AA.
                             Example 1; Col 23; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .3
/label= C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= P
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                    3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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18-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR96137;
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR96137
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The present sequence is a specific example of a fluorogenic substrate for detecting activity of a protease. The substrate agrees with the generic CC detecting activity of a protease. The substrate agrees with the generic CC comparison of the comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease activity; fluorphore; detection; fluorogenic; cellular uptake;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Asp residue is modified by the presence of Fl where Fl is the donor fluorophore 5'-carboxytetramethylrhodamine (C2211)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Cys residue is modified by the presence of F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fluorogenic peptide(s) with fluorophore at each terminus - for detecting protease(s) in biological samples, emit intense visible fluorescence when cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.9%; Score 33; DB 2; Length 9; 50.0%; Pred. No. 1.4e+06; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D-NorFES-A protease inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Norleucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 31; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW82094 standard; peptide; 9 AA.
                                                                                                                                                                                                                        94US-00331383.
                                                                                                                                             95WO-US013936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= Nle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Komoriya A, Packard BS;
                                                                                                                                                                                                                                                                                          ONCO-) ONCOIMMUNIN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-239512/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conformation change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Modified-site
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                                                                                                                                                                                                                        28-OCT-1994;
                                                                                                                                             27-OCT-1995;
WO9613607-A1
                                                                      09-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW82094;
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us-09-761-636a-13.closed.rag

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The present peptide contains a protease binding site. It is used to produce novel reagents whose fluorescence increases in the presence of produce novel reagents whose fluorescence increases in the presence of particular proteases. These fluorescent signal at a visible wavelength when provide a high intensity fluorescent signal at a visible wavelength when they are digested by a protease. The fluorescent indicators have the general formula: F1-C1-P-C2-F2 | (S1) (S2)k where: P is a peptide containing a protease binding site e.g. AAM46560. F1 and F2 or I. C1 and C2 are conformation-determining regions that introduce a conformation-determining regions that introduce a cent other with a separation of less than 100 Angstrom. When n is 1, S1 is joined to the terminal carboxy group of C1 by a peptide bond, and when k is 1, S2 is joined to the terminal carboxy group of C2 by a peptide bond. The protease indicators are used for detecting protease cutivity in a biological sample. The sample is contacted with the indicator and any change in fluorescence is detected, an increase in
                                                                                                                                                                                            Fluorogenic substrates for protease determination - having two closely spaced fluorophores flanking protease binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease detection; peptide cleavage; enzyme activity; fluorogenic; viral infection; cancer metastasis; emphysema; arthritis; thrombosis; baemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.9%; Score 33; DB 2; Length 9; 50.0%; Pred. No. 1.4e+06; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= OTHER
/note= "modified by fluorophore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "modified by fluorophore"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Socation/Qualifiers
                                                                                                                                                                                                                                                       Example 1; Col 23; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG73245 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease indicator peptide #1.
                            94US-00331383,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-2000; 2000WO-US024882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2001 (first entry)
                                                                                                          Packard BS, Komoriya A;
                                                                   (ONCO-) ONCOIMMUNIN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SVPLSVPC 10
                                                                                                                                                   WPI; 1998-158345/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200118238-A1
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Modified-site
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                          28-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG73245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW82023-W82240 are peptides used in the construction of a fluorogenic composition which is used for the detection of protease activity in biological samples. The products can be used for the detection of conformation changes in nucleic acids, oligosaccharides, polyeaccharides, proteins, peptides, lipids, phobbolipids, glycolipids, glycoproteins, steroids or polymers. In addition, attachment of a hydrophobic group to a molecule can be used to enhance uptake by cells. The composition is composed of P = peptide comprising a protease binding site for the protease, F1, F2 peptides = fluorophores where F1 is attached to the amino acid and S1, S2 peptides = when present, are peptide spacers where S1, when present, is attached to the amino terminal acid, and S2, when present, is attached to the amino acid, and S2, when present, is attached to the amino acid, and S2, when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protease binding site; protease; protease indicator; fluorescent signal; detection; protease activity.
                                                                                                                                                                                                                                                                                                                                                New fluorogenic compositions - containing 2 fluorophores separated by a peptide comprising a protease binding site, used for detecting protease
where F2 is the acceptor fluorophore rhodamine X acetamide (R492)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 2; Length 9;
Pred. No. 1.4e+06;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide backbone of a protease indicator,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Nle
/note= "Norleucine"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 10; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW46561 standard; peptide; 9 AA.
                                                                                                                                               98WO-US003000
                                                                                                                                                                                   97US-00802981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00549008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                      Komoriya A, Packard BS;
                                                                                                                                                                                                                             (ONCO-) ONCOIMMUNIN INC.
                                                                                                                                                                                                                                                                                                                                                                                             activity in samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                           IPI; 1998-467579/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::| |:||
2 AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                            WO9837226-A1
                                                                                                                                            20-FEB-1998;
                                                                                                                                                                                      20-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-0CT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5714342-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW46561;
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RESULT 8

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Gaps ·,

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WPI; 2002-698548/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU00643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "F2, where F2 is an acceptor fluorophore rhodamine X acetamide (R492)"
                                                                                                                                     The present invention describes fluorogenic compositions which can be used for the detection of protease activity. This can be useful as an indicator of viral infection, cancer metaersais, haemophilia, emphysema, thrombosis and arthritis. The fluorogenic compositions comprise a peptide, a peptide spacer and a donor and an acceptor fluorophore. The peptide, is cleaved by a protease and the fluorophores can then be detected. The present sequence is one of the peptides described in the exemplification of the invention
                                                                        New fluorogenic compositions whose fluorescence level increases in the presence of active proteases, useful for detecting and localizing protease activity in biological samples, particularly in frozen tissue
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Protease; indicator; chromophore; H-dimer; fluorescence; absorbance; nuclease; screening; fluorophore; substrate cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "F1, where F1 is a donor fluorophore 5'-carbocytetramethylrhodamine (C2211)"
                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                   Score 33; DB 4; Length y;
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      D-NorFES-A protease inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "norleucine"
                                                                                                                       Example 2; Page 53; 86pp; English.
                                                                                                                                                                                                                                                                                                                                               ABU60357 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-2000; 2000US-00747287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2001; 2001WO-US049781
 99US-00394019.
                                                                                                                                                                                                                                            58.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Nle
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.04;
H. Conservative
                                                                                                                                                                                                                                                                                                                                                                                    29-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Packard BS, Komoriya A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ONCO-) ONCOIMMUNIN INC.
                   (ONCO-) ONCOIMMUNIN INC.
                                      Packard
                                                                                                                                                                                                                                                                                3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                            ::| |:||
2 AIPXSIPC 9
                                                       WPI; 2001-389573/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200261038-A2
                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-2002
                                      Komoriya A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                  ABU60357;
                                                                                                      samples.
                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                         ABU6035'
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couply labeled compositions) comprising a polypeptide backbone or a nucleic acid backbone joining two chromophores of the same species couply labeled compositions) comprising a polypeptide backbone or a nucleic acid backbone joining two chromophores of the same species concerned for a change in the absorbance of the chromophore, a decrease in fluorescence or a change in the absorbance indicates that the fluorescence or a change in absorbance indicates that the indicator is cuseful for detecting the activity of a procease, where an increase in fluorescence or a change in absorbance indicates that the protease in fluorescence or a change in absorbance indicates that the protease in fluorescence or a change in absorbance indicates that the protease in fluorescence or a change in absorbance indicates that the protease in fluorescence or a change in absorbance indicator is attached to a solid support inside a mammalian, yeast or insect cell. The composition bears a hydrophobic group such as Fmc. 9-fluoreneacetboxylic group, 1-carboxylic group, 9-flooreneacetboxylic group, 1-carboxylic group, 1-carboxylic group, 1-carboxylity [Mrt], 4-methoxyrtityl [Mrt], 4-methoxyrityl [Mrt], 4-methoxyri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Membrane translocating peptide, MTLP; human; intracellular gene delivery; epithelial cell layer; gastrointestinal tract; circulatory system.
                                                                                                                                                                                                                                                                                                                                                                     (referred as homo-
Indicator composition comprising polypeptide or nucleic acid backbone joining two same chromophores resulting in quenching of fluorescence of/change in absorbance of chromophores, useful for detecting protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel indicator composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human membrane translocating peptide (MTLP) #12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 5; I
Pred. No. 1.4e+06;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU00643 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-2001 (first entry)
                                                                                                                                                                                                                                                             Example 2; Page 15; 97pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 SVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | | | | 2 AIPXSIPC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU00643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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Brayden D;

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O'mahony DJ, Byrne D,
             (OMAH/) O'MAHONY D J.
                                                         WPI; 2003-229409/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU94301;
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                  factor.
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU94301
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                                                                                                                                                                                                                                                          The sequence represents a human membrane translocated peptide (WTLP).

WTLPs and their related fragments, motifs derivatives and analogues are used for enhancing uptake of a pharmaceutically active agent into a cell, into or out of an intracellular compartment and across a cell layer (for example, an epithelial cell layer liming the gastrointestinal tract), either directly or from a pharmaceutically active agent loaded particle, into the circulatory system of an animal. This method is useful for intracellular gene delivery, as a rapid screening method for the identification of MTLPs which retain the functional activity of a MTLP and characterising the properties of a MTLP, for diagnosis of a pathological discorder (by administration of a MTLP-active particle complex comprising a diagnostic agent complex or MTLP-active particle complex comprising a diagnostic agent complex or MTLP-active particle complex comprising a diagnostic agent) and for preventing or treating a pathological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                              Compositions for enhancing uptake of e.g. drugs or DNA across a cell membrane, comprise membrane translocating peptides having specific amino acid sequences or a derivative, fragment, motif, analog or peptidomimetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peyer's patch cell; non-Peyer's patch cell; transcription factor; upregulated protein; antigen; vaccine delivery; M cell; membrane translocating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 4; Length 10; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane translocating peptide #12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADB88786 standard; peptide; 10 AA.
                                                                                                                                                                                                                                     Claim 2; Page 11; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2001; 2001US-0281387P. 02-JUL-2001; 2001US-0302591P.
                                           27-SEP-2000; 2000WO-IB001491.
                                                                 99US-0156246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2002; 2002WO-IB003866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-DEC-2003 (first entry)
                                                                                                                         O'mahony DJ, Lambkin IJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.1
Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CLPVLLAAPC 10
                                                                                       OMAH/) O'MAHONY D J.
                                                                                                  LAMB/) LAMBKIN I J.
                                                                                                                                               WPI; 2001-300212/31.
                                                                                                                                                          N-PSDB; AAS00637.
                                                                                                                                                                                                                 of the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003004646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10 AA;
WO200127154-A2
                                                                27-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2003
                      19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB88786;
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The invention relates to a novel method for increasing the levels of a protein in a Peyer's patch cell. The method comprises delivering to the cell a nucleic acid coding for a protein, the level of which or its mRNA is greater than in a non-Peyer's patch cell. The preferred protein of the cell a nucleic acid coding for a protein, the preferred protein of the is greater than in a non-Peyer's patch cell. The preferred protein of the cell in greater than in a non-Peyer's patch of a protein that activates of the invention is transcription factor of transcription 3, NfKappa&bgr; Tf plo5 signal transducer and activator of transcription 3, NfKappa&bgr; Tf plo5 computer, S-myc prote-oncogene, myc related, Nm3-M2, nucleoside cliphosphate kinase B, metastasis reducing protein, and C-est-I prote-oncogene, and p54. The preferred upregulated protein of the invention is selected from clusterin. T-cell surface glycoprotein CD5 precursor, HSP selected from the group. The method is useful for increasing or a protein in a Peyer's patch cell, particularly in increasing antigen or vaccine delivery to M cells. The method may also the used to enhance transport of a drug through the gastrointestinal tract increasing antigen or vaccine delivery to M cells. The method may also the used to enhance transport of a drug through the gastrointestinal tract increasing minimal tract in the protein of the transport of a drug through the gastrointestinal tract increasing matched the membrane translocating peptide of the
Increasing the levels of a protein in a Peyer's patch cell, useful for targeted vaccine or drug delivery, comprises delivering to the Peyer's patch cell a transcription factor or an activator of a transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2El1; calcium transport protein; cancer; prostate cancer; cytostatic; chromosome 7q34; chromosome 12q24.1; T cell; B cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.1%; Score 32; DB 7; Length 10; 50.0%; Pred. No. 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human novel protein CaTrF2E11 HLA binding peptide #134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raitano AB, Challita-Eid PM, Faris M, Saffran DC,
Levin E, Hubert RS, Ge W, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                          Example 6; Page 51; 147pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-2001; 2001WO-US025782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CISVPLSVPC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200214361-A2.
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21-FEB-2002.

WPI; 2002-269179/31.

Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample. Example 11; Page 173; 270pp; English.

The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7q34) gene products in a biological cample from a patient who has or is suspected of having cancer (sepecially prostate cancer). Comprises: (a) determining the status of 83P2H3 gene products expressed by cells in a tissue sample from an individual and (b) comparing the status to the status of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 correction or status, generating antibodies/immune response against 83P2H3 function or status, generating antibodies/immune response against 83P2H3 correction denitied Hia (human leukocyte antigen) binding peptides derived from the protein, delivering a cytotoxic agent to a cell cerombinant protein comprising an antigen-binding region of the antibody, a recombinant protein comprising an antigen-binding region of the antibody, a recombinant protein, a phyridoma that produces the recombinant protein, a monoclonal antibody that comprises the recombinant protein, a polymicleotide that encodes the monoclonal antibody and inducing an immune response to a 83P2H3 antibody, a vector comprising a content that comprises a T cell or B cell respectively. The method immune response to a 83P2H3 antibody, a vector comprising a susful for monitoring salter of cancer in an individual. The modulator is useful for inhibiting the growth of cancer cells that express 83P2H3. For encoding an antibody is useful for inhibiting the growth of cancer cells that express 83P2H3. For encoding salter and the vector is useful for treating an immune system T cell or B cell, respectively. The method cancer that expresses 83P2H3. The immunological methods are useful for reating an immune response against sapplit) and for detecting the presence of 83P2H3. The immunological methods are useful for amplituation and treatment, to detect and quantify sand mutant cancer that expresses 83P2H3. The immunological isolating 83P2H3 homologues/related molecules, and for generating anti-idiotypic antibodies that mimic the 83P2H3 protein. The present sequence is an HLA binding peptide motif from 83P2H3 or its related protein

Sequence 9 AA;

Gaps ; Length 9; 1; Indels 56.2%; Score 31.5; DB 5; 60.0%; Pred. No. 1.4e+06; ive 2; Mismatches 1; 6; Conservative Local Similarity Query Match Matches

1;

1 CISVPLSVPC 10 |:: ||| || 1 CLT-PLSFPC 9

ð 임

AAU94201 standard; peptide; 10 AA. 02-JUL-2002 (first entry) AAU94201; RESULT 14 AAU94201

Human novel protein CaTrF2E11 HLA binding peptide #84.

Human, human leukocyte antigen; HIA; immunogen; 83P2H3; CaTrF2Ell; calcium transport protein; cancer; prostate cancer; cytostatic; chromosome 7q34; chromosome 12q24.1; T cell; B cell.

WO200214361-A2.

```
The invention relates to monitoring 8322H3 (a calcium transport protein whose gene is located on chromosome 7q34) gene products in a biological ample from a patient who has or is suspected of having cancer (especially prostate cancer), comprises: (a) determining the status of 83P2H3 gene products expressed by cells in a tissue sample from an individual and (b) comparing the status to the status of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 correction or status, generating antibodies/immune response against 83P2H3 (or related protein Carryzzzii whose gene is located on chromosome capressing 83P2H3 by conjugating the agent to a cell carryzed from the protein dalivering a cytotoxic agent to a cell carryzed in 83P2H3 by conjugating the agent to an anti-83P2H3 antibody, a recombinant protein comprising an antigen-binding region of the antibody, a recombinant produces the recombinant protein, a produces the recombinant protein, a produces the recombinant protein, a comprises the variable domains of the heavy and connoclonal antibody that comprises the variable domains of the heavy and light chains of the anti-83P2H3 antibody a vector comprising a polymucleotide that encodes the monoclonal antibody and inducing an immune system T cell or B cell, respectively. The method is useful for monitoring 83P2H3 gene products in a biological sample for monitoring the presence of cancer in an individual. The modulator is useful for inhibiting the growth of cancer cells that express 83P2H3, for treating cancer and the vector is useful for treating an immune response against 83P2H3, and for detecting the presence of cancer in an individual. The modulator is useful for an expense 83P2H3. The immunological methods are useful for semence of 83P2H3-related protein or polymucleotide in a biological method are useful for an expense sample for the holds or polymoleotide in a biological method is useful for an expense against 83P2H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibody is useful in prostate cancer diagnosis, prognosis, imaging methodologies and treatment, to detect and quantify 83PSH3 and mutant 83PSH3-related proteins, for purifying a 83P2H3-related protein, for isolated protein, for isolatypic antibodies that mimic the 83P2H3 protein. The present sequence is an HLA binding peptide motif from 83P2H3 or its related protein
                                                                                                                                                                                                                                                                                                                                                     Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample.
                                                                                                                                                                                                                             Saffran DC, Afar DEH;
                                                                                                                                                                                                                          -Eid PM, Faris M, Sa
Ge W, Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 11; Page 169; 270pp; English.
                                                                                                                                                                                                                                  Challita-Eid PM,
                                                                      17-AUG-2001; 2001WO-US025782.
                                                                                                                          17-AUG-2000; 2000US-0226329P.
                                                                                                                                                                                                            Raitano AB, Charry Hubert RS,
                                                                                                                                                                            (AGEN-) AGENSYS INC.
                                                                                                                                                                                                                                                                                                         WPI; 2002-269179/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10 AA;
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Gaps ï DB 5; Length 10; 1; Indels 2; Mismatches 56.2%; Score 31.5; 60.0%; Pred. No. 99; 6; Conservative 1 CISVPLSVPC 10 |:: ||| || 1 CLT-PLSFPC 9 Best Local Similarity Matches 6; Conserve Query Match RESULT 15 AAU94811
ID AAU9
XX
AC AAU9 à

AAU94811 standard; peptide; 10 AA.

AAU94811;

1;

02-JUL-2002 (first entry)

Human novel protein CaTrF2E11 HLA binding peptide #394.

Human; human leukocyte antigen; HLA; immunogen; 83P2H3; CaTrF2El1; calcium transport protein; cancer; prostate cancer; cytostatic; chromosome 7q34; chromosome 12q24.1; T cel1; B cel1.

Homo sapiens.

WO200214361-A2,

21-FEB-2002.

L7-AUG-2001; 2001WO-US025782.

17-AUG-2000; 2000US-0226329P.

(AGEN-) AGENSYS INC.

Saffran DC, Afar DEH; Raitano AB, Challita-Eid PM, Faris M, Sa Levin E, Hubert RS, Ge W, Jakobovits A;

WPI; 2002-269179/31.

Monitoring 83P2H3 gene products for monitoring the presence of cancer in a subject, comprises determining the status of 83P2H3 gene products in a tissue sample from the subject and comparing it to a normal sample.

Example 11; Page 191; 270pp; English.

The invention relates to monitoring 83P2H3 (a calcium transport protein whose gene is located on chromosome 7q34) gene products in a biological sample from a patient who has or is suspected of having cancer (especially prostate cancer). Comprises (a) determining the status of 83P2H3 gene products expressed by cells in a tissue sample from an individual and (b) comparing the status to the status of 83P2H3 gene products in a normal sample. Also included are modulators of 83P2H3 correction or status, generating antibodices/immune response against 83P2H3 (or related protein CarrP2EL1 whose gene is located on chromosome 12q24.1) using identified H1A (human leukocyte antigen) binding peptides derived from the protein, delivering a cytocoxic agent to a cell 2q24.1) using identified H1A (human leukocyte antigen) binding peptides derived from the protein, delivering a cytocoxic agent to a cell 2q24.1) using identified H1A (human leukocyte antigen) binding peptides derived from the protein comprising an antigen-binding region of the antibody, a recombinant protein comprising an antigen-binding region of the antibody, a recombinant protein, a single-chain monoclonal antibody that comprises the wariable domains of the heavy and light chains of the anti-83P2H3 antibody, a vector comprising an immune response to a 83P2H3 antibody, a vector comprising an immune response to a 83P2H3 antibody, a vector comprising of protein that comprises a T cell or B cell epitope, and contacting the presence of cancer in an individual. The modulator is useful for monitoring 183P2H3 gene products in a biological sample for monitoring the vector is useful for the growth of cancer cells that expresses 83P2H3. The immune response against 83P2H3, and concacting the cancer that expresses 83P2H3. and cancer that expresses 83P2H3 and cancer disponse to a batient with a sample from a patient who has or who is suspected of having cancer. The sample from a patient who has or who is suspected of having cancer. The companied of the sample from enthodologi solating 83P2H3 homologues/related molecules, and for generating anti-diotypic antibodies that mimic the 83P2H3 protein. The present sequence an HLA binding peptide motif from 83P2H3 or its related protein antibody is useful in prostate cancer diagnosis, prognosis, imaging methodologies and treatment, to detect and quantify 83P2H3 and mutant 83P2H3-related proteins, for purifying a 83P2H3-related protein, for

Sequence 10 AA;

DB 5; Length 10; 56.2%; Score 31.5; I 60.0%; Pred. No. 99; Best Local Similarity Query Match

Gaps ä Indels ;; Mismatches 2; 6; Conservative 1 CISVPLSVPC 10 1 CLT-PLSFPC Matches ð 셤

Search completed: March 8, 2004, 12:44:44 Job time : 53 secs

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Cgm2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

(Ggm2 6/ptodata/2/pubpaa/PGT_NEW_PUB.pep:*

(Ggm2 6/ptodata/2/pubpaa/SGE_NEW_PUB.pep:*

(Ggm2 6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

(Ggm2 6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

(Ggm2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

(Ggm2 6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    809742 seqs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                          US-09-761-636A-13
56
                                                                                                                                                                                                                                                                                                                    1 CISVPLSVPC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 10
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 13. Appl	Sequence 14. Appl	Sequence 13. Appl	Sequence 71, Appl	Sequence 101 App	Sequence 284. App	Seguence 184. Ann	Segmence 560. Ann	Segmence 794. Ann	Sequence 11221. A	Sequence 679, App	Segmence 1006 An	Sequence 1214. An	Semience 1011 An	Sequence 66, Appl
SUMMARIES		QI	US-09-761-636A-13	US-09-761-636A-14	US-10-126-845-13	US-10-126-845-71	US-10-116-275-101	US-09-932-165-284	US-09-932-165-184	US-09-932-165-560	US-09-932-165-794	US-10-154-884B-11221	US-09-932-165-679	US-09-932-165-1006	US-09-932-165-1214	US-09-833-245-1011	US-09-756-283A-66
		8	9	σ	14	14	15	10	10	10	10	15	10	10	10	11	σ
	f Query	Length	10	9	10	10	10	6	10	10	10	σ	on	σ	σ	10	8
d	Query	Match	100.0	74.1	57.1	57.1	57.1	56.2	56.2	56.2	56.2	55.4	53.6	53.6	53.6	51.8	48.2
		Score	99	41.5	32	32	32	31.5	31.5	31.5	31.5	31	30	30	30	29	27
	Result	No.	1	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15

Segmence 11228. A	1125	1125		1125		1127	1128	(1)	43,	Sequence 11276. A	1128	2	2	Ŋ	Sequence 5. Appli	0				12,	3	456,	577	12, 4	37.	a	577	9790	984
15 US-10-154-884B-11228	US-10-154-884B-1	15 US-10-154-884B-11254	15 US-10-154-884B-11258	15 US-10-154-884B-11259	15 US-10-154-884B-11265	15 US-10-154-884B-11275	US-10-15	9 US-09-852-424~32	9 US-09-852-424-43	15 US-10-154-884B-11276	15 US-10-154-884B-11287	-761-636A-10	9 US-09-922-261-21	-135	10 US-09-886-135-5	14 US-10-040-862-9790	14 US-10-040-862-9847	US-10	14 US-10-040-862-10196	14 US-10-277-292-12	14 US-10-277-292-37	14 US-10-277-292-456	14 US-10-277-292-577	15 US-10-280-340-12	15 US-10-280-340-37	15 US-10-280-340-456	15 US-10-280-340-577	15 US-10-057-475B-9790	15 US-10-057-475B-9847
on	σ	6	σ	9	6	σ	6	6	0	თ	σ	σ	10	Ŋ	Ŋ	6	თ	σv	σ	σ	σ,	o	σ,	6	o	6	σ	0	σ
48.2	48.2	48.2	48.2	48.2	48.2	48.2	48.2	46.4	46.4	46.4	46.4	44.6	44.6	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9	42.9
27	27	27	27	27	27	27	27	56	56	56	56	25	52	24	24	24	24	24	24	24	24	24	54	24	24	24	24	24	24
16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-09-761-636A-13

; Sequence 13, Application US/09761636A
; Patent No. USZ0020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: ACHEN, Marc
; APPLICANT: HUGHES, Richard
; APPLICANT: HUGHES, Richard
; APPLICANT: HUGHES, Richard
; APPLICANT: ENEVERNORM, Angela
; TITLE OF INVENTIONS, VEGEO Achen et al
; TITLE OF INVENTIONS, VEGEO Achen et al
; CURRENT FILING DATE: 2001-01-18
; FRIOR APPLICATION NUMBER: US 60/176,293
; FRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR APPLICATION NUMBER: US 60/204,590
; RROR PRILING DATE: 2000-05-16
; SEQ ID NO 13
; LENGTH: 10
; SEQ ID NO 13
; LENGTH: 10
; CARANISM: Homo sapiens
US-09-761-636A-13

QUETY MAtch

Best Local Similarity 100.0%; SCORE 56; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
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Db 1 CISVPLSVPC 10

1 CISVPLSVPC 10

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RESULT 2 US-09-761-636A-14 ; Sequence 14, Application US/09761636A ; Patent No. US20020065218A1

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US-09-932-165-284
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US-10-126-845-13
US-10-126-845-13
Sequence 13, Application US/10126845
Publication No. US20030181367A1
GENERAL INFORMATION:
APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imeded J.
APPLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRARE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFREENCE: E1667/20058
CURRENT RPLICATION UNDER: 2002-10-15
UNUMBER OF SEQ ID NOS: 119
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Pinilla, Clemencia
APPLICANT: Pinilla, Clemencia
APPLICANT: Houghten, Richard
TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
FILE REFERENCE: E1067/20058
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            APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: BUGHES, Richard
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION WUMBER: US/09/761,636A
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.5; DB 9; Length 9
Pred. No. 7.2e+05;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
, OTHER INFORMATION: membrane translocating peptide, cyclic US-10-126-845-13
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US-10-126-845-71
; Sequence 71, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 74.1%;
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CLPVLLAAPC 10
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                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM; Homo sapiens
US-09-761-636A-14
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
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US-10-116-275-101
; Sequence 101, Application US/10116275
; Publication Wo. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Blan Pharmaceutical Technology
; APPLICANT: Brayden, Daniel J.
APPLICANT: Brayden, Daniel J.
APPLICANT: Brayden, Daniel J.
APPLICANT: Hapkin, Inelda
; APPLICANT: Hapkin, Liaa
; APPLICANT: Hapkin, Liaa
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; TURENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 101
LEMOTH: 10
; WANDER OF SEQ ID NOS: 349
; SOFTWARE: Patentin Version 3.1
; EMOTH: 10
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Pred. No. 81;
2; Mismatches 3; Indels
CURRENT APPLICATION NUMBER: US/10/126,845
CURRENT FILLING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 119
SOCTWARE: Patentin version 3.1
LENGTH: 10
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                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
| LOCATION: (1)...(10)
| OTHER INFORMATION: D form amino acid
US-10-126-845-71
                                                                                                                                                                                              FEATURE: OTHER INFORMATION: D form peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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50.0%;
                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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APPLICANT: FARIS, MARY
APPLICANT: ASPERAN, DOUGLAS
APPLICANT: ASPERAN, DOUGLAS
APPLICANT: ASPERAN, DOUGLAS
APPLICANT: LEVIN, ELAN
APPLICANT: LEVIN, ELAN
APPLICANT: LEVIN, ELAN
APPLICANT: GE, WANGMAO
APPLICANT: JAKOBOVITS, AYA
TITLE OF INVENTION: BYPERI AND CATFFZEII USFUL IN TREATMENT AND
TITLE OF INVENTION: BYPERION OF CANCER
FILE REPREMENT: 105/09/932,165
CURRENT APPLICATION NUMBER: 105/09/932,165
CURRENT APPLICATION NUMBER: 60/226,329
PRIOR PRILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SSEQ ID NOS: 1508
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-560
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2; Mismatches
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Publication No. US20030134784A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHALLITY EID, PIA M. FARIS, MARY SAFFRAN, DOUGLAS AFAR, DANIEL LEVIN, ELANA HUBERT, RENE
                                                                                                                                                                                     CHALLITA-EID, PIA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                No. US20030134784A1
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ORGANISM: Artificial Sequence
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CLT-PLSFPC 9
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: SAFRAN, DOUGLAS
APPLICANT: SAFRAN, DOUGLAS
APPLICANT: AFAR, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: LEVIN, ELANA
APPLICANT: LEVIN, ELANA
APPLICANT: LEVIN, ELANA
APPLICANT: JAKOBOVITS, ANA
ITILE OF INVENTION: WIGHERT ACTIVE AND CORRESPONDING PROTEINS ENTITLED
ITILE OF INVENTION: B3P2H3 AND CATFEELI USBFUL IN TREATMENT AND
ITILE OF INVENTION: B3P2H3 AND CATFEELI USBFUL IN TREATMENT AND
ITILE OF INVENTION: WIGHER: US/09/932,165
CURRENT FILING DATE: 2001-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PEACHLIN Ver. 2.1
IENSTH: 10
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US-09-932-165-184
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Pred. No. 97;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 56.2%; Score 31.5; DB 10; Length 9; Similarity 60.0%; Pred. No. 7.2e+05; 6; Conservative 2; Mismatches 1; Indels
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Publication No. US20030134784A1
GENERAL INFORMATION:
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
APPLICANT: FARIS, MARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 560, Application US/09932165
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60.0%;
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ORGANISM: Artificial Seguence
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ORGANISM: Artificial Sequence
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Best Local Similarity 60.0
Matches 6; Conservative
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1 CLT-PLSFPC 9
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1 CLT-PLSFPC 9
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Best Local Similarity
Matches 6; Conserva
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US-09-932-165-560
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Gaps

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Indels

Length 10;

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APPLICANT: JAKOBOVITS, ANA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: 812P1A AND CATFFZELI USEFUL IN TREATMENT AND
TITLE OF INVENTION: 018P2TCTION OF CANCER
FILE REPERENCE: 51158-20014.00
CURRENT APPLICATION NUMBER: 105/09/932,165
CURRENT FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR PLICATION NUMBER: 60/226,329
NUMBER OF SEQ ID NOS: 1508
SOFTWARE: PATENTION VET: 2.1
SEQ ID NO 794
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Best Local Similarity 60.0%; Pred. No. 97;
Matches 6; Conservative 2; Mismatches
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APPLICANT: SAFRAN DOUGLAS
APPLICANT: SAFRAN DOUGLAS
APPLICANT: SAFRAN DOUGLAS
APPLICANT: ARA, DANIEL
APPLICANT: BLANA
APPLICANT: HUBERT, RENE
APPLICANT: GE, WANGRAO
APPLICANT: GE, WANGRAO
APPLICANT: ACADEMICAN BLANA
TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
TITLE OF INVENTION: B3PRH3 AND CARFZELI USEFUL IN TREATMENT AND
TITLE OF INVENTION: B3PRH3 AND CANCER
FILE REFRENCE: 51158-20014.00
CURRENT APPLICANTON NUMBER: 60/99/332,165
CURRENT FILING DATE: 2001-08-17
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 1508
SEQ ID NOS: 1508
SEQ ID NO 1006
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TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED TITLE OF INVENTION: 83P2H3 AND CATYPZELI USEFUL IN TREATMENT AND TITLE OF INVENTION: DETECTION OF CANCER FILE REFERENCE: 51158-20014.00 CURRENT APPLICATION NUMBER: US/09/932,165
CURRENT PILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/226,329
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 1508
SSOFTWARE: PARENTIN Ver: 2.1
SSQ ID NO 679
LENGTH: 9
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US-09-932-165-1006
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CRANISM: Artificial Sequence
FRATURE:
CONTRR INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 53.6%; Score 30; DB 10; Length 9; Best Local Similarity 83.3%; Pred. No. 7.2e+05; Matches 5; Conservative 0; Mismatches 1; Indels
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US-09-932-165-1214
US-09-932-165-1214
; Sequence 1214, Application US/09932165
; Publication No. US20030134784A1
; GENERAL INFORMATION:
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Publication No. US20030134784A1
GENERAL INFORMATION:
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APPLICANT: CHALLITA-EID, PIA M.
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US-10-154-84818-11221
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US-10-154-84818-11221
US-10-154-84818-1122
US-10-154-84818-1122
US-10-154-84818-1123
US-10-154-84818-1123
US-10-154-84818-1123
US-10-154-84818-1123
US-10-154-84818-1133
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Publication No. US20030134784A1
GENERAL INFORMATION, ARTHUR
APPLICANT: RAITANO, ARTHUR
APPLICANT: CHALLITA-EID, PIA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FARIS, MARY
SAFFRAN, DOUGLAS
AFAR, DANIEL
LEVIN, ELANA
HUBERT, RENE
GE, WANGMAO
JAKOBOVITS, AYA
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Best Local Similarity 71.4
Matches 5; Conservative
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US-10-154-884B-11221
                                                                       1 CISVPLSVPC 10
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CLT-PLSFPC 9
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2 CLSVPVS 8
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JS-10-154-884B-11221
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US-09-932-165-679
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                       FEATURE:
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         APPLICANT: GE, WANGWAO

APPLICANT: GE, WANGWAO

TITLLE OF INVENTION: UGLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED

TITLLE OF INVENTION: B3P2H3 AND CATEPELL IN TREATMENT AND

TITLE OF INVENTION: DETECTION OF CANCER

TITLE OF INVENTION: DETECTION OF CANCER

TITLE OF INVENTION: DETECTION OF CANCER

CURRENT APPLICATION NUMBER: US/09/932,165

CURRENT APPLICATION NUMBER: 60/226,329

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 1508

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1214

LENGTH: 9

TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.6%; Score 30; DB 10; Length 9; Best Local Similarity 83.3%; Pred. No. 7.2e+05; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Publication No. US200400134A1

Sequence 1011, Application US/09833245

Publication No. US20040010134A1

SERVELAI INFORMATION:
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFRENCE: PF546PCT
CURRENT APPLICATION NUMBER: 05/029, 358

PRIOR APPLICATION NUMBER: 06/229, 358

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-15

NUMBER OF SEQ ID NOS: 2267

SEQ ID NO 1011

LENGTH: 10
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US-09-756-283A-66
; Sequence 66, Application US/09756283A
; Patent No. US20020151478A1
RAITANO, ARTHUR
CHALLITA-EID, PIA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-833-245-1011
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; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Dadams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFRENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT TILING DATE: 2001-01-09
; VUMBER OF SEQ ID NOS: 100 NOS: 100
; SOFTWARE: PatentIn version 3.0
; Table version 3.0
; SOFTWARE: PatentIn version 3.0
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; Table version 3.0
; Table version 3.0
; Table version 3.0
; SOFTWARE: PatentIn version 3.0
; Table version 3.0
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Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 1375, Ap
Sequence 1375, Ap
Sequence 1375, Ap
Sequence 1391, Ap
Sequence 1391, Ap
Sequence 3574, Ap
Sequence 3574, Ap
Sequence 11, Appl
Sequence 1140, Ap
Sequence 2155, Ap
                                                                        March 8, 2004, 12:28:28; Search time 22 Seconds (without alignments) 16.426 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                    1: /cgm2 6/ptodata/2/jaa/5A COMB.pep:*
2: /cgm2 6/ptodata/2/jaa/5B-COMB.pep:*
3: /cgm2 6/ptodata/2/jaa/6A COMB.pep:*
4: /cgm2 6/ptodata/2/jaa/6A COMB.pep:*
5: /cgm2 6/ptodata/2/jaa/PCTUS COMB.pep:*
6: /cgm2 6/ptodata/2/jaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-62-85-21
US-09-226-985-21
US-09-227-906-21
US-09-187-859-1375
US-09-187-859-1375
US-09-187-859-1375
US-09-187-859-3971
US-09-187-859-4647
US-09-187-859-4647
US-09-187-859-4647
US-09-187-859-4647
US-09-187-859-1392
US-09-187-859-1392
US-09-187-859-1392
US-09-187-859-1392
US-09-187-859-2726
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US-09-839-542B-1740
US-09-839-542B-2155
US-09-839-542B-2720
US-09-839-542B-3637
                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                   389414 seqs, 51625971 residues
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                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Match Length
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1 CVPLTSC 7
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Perfect score:
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28 23 54.8 7 4 US-09-839-542B-4041 Sequence 4041, 29 23 54.8 7 4 US-09-535-652-1026 Sequence 1826, 31 22 52.4 4 2 US-08-429-964-41 Sequence 41, 2 S-4 4 4 US-09-663-8624-35 Sequence 41, 3 Sequence 41, 2 S-4 4 5 PCT-US39-00602-41 Sequence 41, 3 Sequence 26, 3 S-2 52.4 7 1 US-07-958-903A-26 Sequence 26, 3 S-2 52.4 7 1 US-07-958-903A-26 Sequence 26, 3 S-2 52.4 7 1 US-08-823-245-26 Sequence 26, 3 S-2 52.4 7 4 US-07-963-1288 Sequence 26, 3 S-2 52.4 7 4 US-07-963-1288 Sequence 26, 3 S-2 52.4 7 4 US-09-187-859-188 Sequence 3621, 4 US-09-187-859-360 Sequence 3621, 4 US-09-187-859-361 Sequence 3621, 4 US-09-187-859-362 Sequence 3621, 4 US-09-187-859-362 Sequence 3621, 4 US-09-839-542B-188 Sequence 3621, 4 US-09-839-542B-188 Sequence 3621, 4 US-09-839-542B-188 Sequence 3666, 4 US-09-839-542B-3621 Sequence 3666, 4 US-09-839-842B-3621 Sequence 3666, 4 US-09-839-842B-3621 Sequence 3666, 4 US-09-839-842B-3621 Sequence 3666, 4 US-09-839-842B-3621 Sequence 3666, 4 US-09-839-8	Ap Ap	[dd	Appl Appl	Appl Appl , Ap	4444	Ap A
23 54.8 7 4 US-09-839-542B-4041 Sequence 2 55.4 4 US-09-535-852-1826 Sequence 2 52.4 4 US-09-535-852-1826 Sequence 2 52.4 4 US-09-65-362A-35 Sequence 2 52.4 4 US-09-65-362A-35 Sequence 2 52.4 7 1 US-09-69-903A-26 Sequence 2 52.4 7 1 US-08-822-24-26 Sequence 2 52.4 7 1 US-08-822-24-26 Sequence 2 52.4 7 1 US-08-822-24-26 Sequence 2 52.4 7 4 US-09-187-859-188 Sequence 2 52.4 7 4 US-09-187-859-188 Sequence 2 52.4 7 4 US-09-187-859-366 Sequence 2 52.4 7 4 US-09-839-542B-360 Sequence 2 52.4 7 4 US-09-839-542B-361	1041,			6, 7 6, 7 888,	750, 606, 621,	
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222 222 222 222 222 222 222 222 222 22	US-09-839-542B-4041 US-09-535-852-1826	US-08-429-964-41 US-09-665-362A-35 PCT-TIS93-08062-41	US-07-958-903A-26 US-08-462-018-26	US-08-823-245-26 US-07-963-329A-26 US-09-187-859-1888	US-09-187-859-2750 US-09-187-859-3606 US-09-187-859-3621 US-09-839-5428-1888	US-09-839-542B-2750 US-09-839-542B-3606 US-09-839-542B-3621 US-09-535-852-918
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	28 29	30 32 32	33 34 74	9 9 9 6 9 9 7 4 6 9	2 W 4 4. 0 Q O U	4 4 4 4 ሪ

ALIGNMENTS

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Sequence 21, Application US/08526710
Patent No. 562269
GBNERAL INPORMATION:
APPLICANT: Ruoslalti, Erkki
APPLICANT: Ruoslalti, Renata
TITLE OF INVENTION: Method of Identifying Molecules That
TITLE OF INVENTION: Home to a Selected Organ In Vivo
NUMBER OF SECURNCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.8%; Score 31; DB 1; Length 7; 57.1%; Pred. No. 3e+05; ive 2; Mismatches 1; Indels
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SURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/526,710
FILLING DATE: 11-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRANCE/DOCKET NUMBER: P-LJ 1779
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ. 1D NO: 21:
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 4370 La John Vi
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
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Best Local Similarity
Matches 4; Conserv
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MOLECULE TYPE: peptide
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Matches 4; Conserv
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1 CLPVASC 7
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Fatent No. 629632
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Renata
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
ADDRESSEE: Campbell & Flores Lip
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COMPTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
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                     Sequence 21, Application US/08862855

| Sequence 21, Application US/08862855
| Patent No. 606829
| GENERAL INFORMATION:
| APPLICANT: Reagualini, Renata TITLE OF INVENTION: Method of Identifying Molecules That TITLE OF INVENTION: Home to a Selected Organ In Vivo NUMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS:
| ADDRESSEE Campbell & Flores LLP STREET 4700 La Joila Village Drive, Suite 700 STATE: California COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
OPERATING SYSTEM: PC-DOS/NS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 11-SEP-1995

FILING DATE: 10-MAR-1997
APPLICATION DATA: 08/813,273
APPLICATION NUMBER: US 08/813,273
ATORNEY/AGENT INFORMATION:
ARGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-9001
INPORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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1 CLPVASC 7
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RESULT 2
US-08-862-855-21
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US-09-226-985-21
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Patent No. 6306365

GENERAL INFORMATION:

APPLICANT: Rucelahti, Erkki

APPLICANT: Pasqualini, Renata

TITLE OF INVENTION: Method of Identifying Molecules That

TITLE OF INVENTION: Home to a Selected Organ In Vivo

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States
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MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
COMPUTER: IBN PC compatible
COMPUTER: PROPER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
MEDIUM TYPE: Floppy disk
COMPUTER: IMP PC compatible
CONFLYING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDERS:
TILING DATE: 10-MRA-1957
PRIOR APPLICATION NUMBER: US 08/813,273
PRIOR APPLICATION NUMBER: US 08/862,855
FILING DATE: 23-MAX-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERRANCE/DOCKET NUMBER: 9-LJ 3423
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9901
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/526,710
FILING DATE: 11-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/813,273
FILING DATE: 10-MAR-1997
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1375
LENGTH: 7
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US-09-187-859-3971
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GENERAL INFORMATION:

APPLICANT: Blaschuk, Orest W.

APPLICANT: Blaschuk, Orest W.

APPLICANT: Burbara U.

TITLE OF INVENTION: CAMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

TITLE OF INVENTION: CAMPURIN-MEDIATED FUNCTIONS

TITLE OF INVENTION: CAMPURIN-MEDIATED FUNCTIONS

CURRENT APPLICATION NUMBER: US/09/187,859A

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052
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Batent No. 656996
GENERAL INFORMATION.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAMPHONIN MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICANTION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/862,855
PILLING DATE: 23-MAY-1997
ATTORNEY ARENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,415
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-901
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1375, Application US/09187859A Patent No. 6358920
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ORGANISM: Artificial Sequence
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amino acid
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-227-906-21
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserved
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US-09-839-542B-1375
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US-09-187-859-1375
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Patent No. 6358920

GENERAL INPORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL:
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERRINCE: 100066.4071.
GURRENT APPLICATION NUMBER: US/09/187,859A

GURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1799
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADBERIA-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT ERLING DATE: 1999-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3971
                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence US-09-839-542B-1375
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59.5%; Score 25; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 3; Indels
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57.1%; Pred. No. 3e+05;
tive 0; Mismatches
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Patent No. 6358920
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 57.18
Matches 4; Conservative
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4; Conservative
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Matches 4; Conserv
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                   RESULT 11
JS-09-839-542B-3971
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; Sequence 1799, Application US/09839542B
; Patent No. 656996
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL.
; TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 1006066, 407D1.
; CURRENT FILING DATE: 2001-04-20
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 4052
; SEQ ID NO: 405.
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                                           Gaps
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APPLICANT: Blastow, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPRENCE: 100006.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
UUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4047
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OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.5%; Score 25; DB 4; Length 7; 57.1%; Pred. No. 3e+05;
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59.5%; Score 25; DB 4; Length 7; 57.1%; Pred. No. 3e+05; 1ive 0; Mismatches 3; Indel8
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ORGANISM: Artificial Sequence
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    Query Match 59.5
Best Local Similarity 57.1
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserva
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Matches 4; Conserv
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US-09-839-542B-1799
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US-09-839-542B-4047
is Sequence 4047, Application US/09839542B
is Patent No. 656996
gransral invorant.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE RERERENCE: 1000664.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NOS: 4052
LEMETRY APPLICATION OF THE CONTRACT OF THE CONTRAC
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                                                                                             GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAMPENIA. MEDIATED FUNCTIONS
FILE REPERRANCE: 100086, 407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARR: Patentin Ver. 2.0
SEQ ID NO 3971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Representative cyclic modulating agent based on ; OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-09-839-542B-3971
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59.5%; Score 25; DB 4;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches
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57.1%; Pred. No. 3e+05;
tive 0; Mismatches
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US-09-187-859-3574
; Sequence 3574, Application US/09187859A
; Patent No. 6388920
; GENERAL INFORMATION:
Sequence 3971, Application US/09839542B Patent No. 6569996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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TOPOLOGY: linear
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US-09-839-542B-3574

i Sequence 3574, Application US/09839542B

i Patent No. 656996

i GENERAL INFORMATION:

i APPLICANT: Symonda James Matthew

APPLICANT: Symonda James Matthew

i TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

I TITLE OF INVENTION: CAPHERIA-MEDIATED FUNCTIONS

I TITLE OF INVENTION: CAPHERIA-MEDIATED FUNCTIONS

FILE REPRENCE: 100086.40701

CURRENT FILIG DATE: 2001-04-20

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 3574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADEBRAY-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
COTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion COTHER INFORMATION: recognition sequence
US-09-839-542B-3574
                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Representative cyclic modulating agent based on ...
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion ...
US-09-187-859-3574
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APPLICANT: Walton, Paul E.
APPLICANT: Ballard, Francis J.
APPLICANT: McMurty, John P.
APPLICANT: Phelps, Patricia V.
TITLE OF INVENTION: Method of Administering IGF-1, IGF-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
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; Sequence 13, Application US/07947035
; Patent No. 544045
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 42.9
Matches 3; Conservative
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Best Local Similarity
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1 CDPVSGC 7
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                                                                                                                                                                                                               SEQ ID NO 3574
                                                                                                                                                                                                                                       LENGTH
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rTITE OF INVESTION: and Analogs Thereof to Birds
NUMBER OF SURENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE Kenner D. Sibley
STREET: P.O. Drawer 34009
GITY: Charlotte
GITYRY: US
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BATCHIN Release #10. Version #1.30
GITRAT APPLICATION DATA:
APPLICATION NUMBER: US/07/947,035
FILING DATE: 17-SEP-1992
CLASSIPICATION: S14
ATTORNEY/AGRATINON NUMBER: 31.65
REPRENCE/DOCKET NUMBER: 31.65
REPRENCE/DOCKET NUMBER: 5175-59
TELEFAN: (919) 881-3176
TELEFAN: (919) 881-3175
TELEFAN: (910) 881-3175
TELEFAN: (910)
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us-09-761-636a-12.closed.rpr

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March 8, 2004, 12:35:19; Search time 21 Seconds (without alignments) 27.483 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                 316
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                      283366 segs, 96191526 residues
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                      US-09-761-636A-12
                                                                                                                                                                                                                            1 CVPLTC 6
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                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                            Sequence:
                                                                                                            Run on:
                                                                                                                                                                                      Title:
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Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

PIR 78:* Database

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

R-phycoerythrin all metallothionein-A Ig mu chain V regi pallidipin - assas addium-binding pe acid proteinase li protamine Pl - gor MHC H2-K-k cell su T-cell receptor be T-cell receptor ga R-phycoerythrin al major protein anti R-phycoerythrin ga laminin Bl - weste tyrosine-melanocyt glycoprotein compo R-phycoerythrin be halo-toxin - Pseud lipopeptide WS1279 schwannomin - mous glycogen phosphory hemoglobin, extrac phosphoprotein, bo contraction-inhibi - human angiotensin-conver - malaria Description protein actin I SUMMARIES I49421 A32039 I54357 A60521 I37263 C22565 A22565 I51049 S43959 S55238 B37988 B45525 S65726 S11127 A61049 JU0355 PQ0008 A27696 I67345 PT0652 F41946 H48394 В Query Match Length Score Result No. 222 222 223 234 236 237 237 238

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Gaps

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major protein antigen MPT63 - Mycobacterium tuberculosis (fragment) C;Species: Mycobacterium tuberculosis

S 2 VPLT 5

RESULT 3

Na+/K+-exchanging hypothetical TCL3	rylosine plotein A proctolin - Americ peptidyl-dipeptida	peptidyl-dipeptida flagellar protein	angiotensin-conver	hypothetical prote		thyroliberin - she	thyroliberin - eas thyrotropin-releas
6 2 S29881 6 4 I79564 3 3 I78890	5 1 HOROHA 5 2 JN0862	5 2 E42364	5 2 PQ0009 5 2 A60411	5 2 S53595 6 4 A35039	3 3 RHTDTO 3 3 RHPGT	3 3 RHSHT	3 3 A33802
9 23.7 9 23.7 8 21.1		8 21.1	8 21.1 8 21.1	8 21.1 8 21.1	7 18.4 7 18.4	7 18.4	7 18.4
30 31 32	8 8 9 8 4 1	36	37 38	39 40	41 42	43 44 44	t 4.

ALIGNMENTS

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C;Species: Mas musculus (house mouse)
C;Species: Mas musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 165546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
A;Title: Detailed analysis of the mouse H-2xb promoter: Enhancer-like sequences and the A;Reference number: 152778; MUID:86106202; PMID:3510743
A;Accession: 165546
A;Accession: 165546
A;Molacule type: DNA
A;Residues: 1-6 -RES>
                                                                                                                                                                                                                                                                                                                                                                                                    0;
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)
C.Species: Gastroclonium coulteri
C.Jate: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
                                                                          C,Accession: B22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4885-4863, 1988
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234
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0
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                                                                                                                                                                                                                                                                                                                                           Length 5;
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                                                                                                                                                                                                                                                                                                                               52.6%; Score 20; DB 2; Le
100.0%; Pred. No. 2.8e+05;
.ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHC H2-L antigen - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                        A;Accession: B22565
A;Molecule type: protein
A;Residues: 1-5 <KLO>
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Matches
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C;Accession: A60521
R;Bonamusa, L.; Baanante, L.V.
R;Bonamusa, L.; Baanante, L.V.
A;Denamusa, L.; Baanante, L.V.
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mt
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mt
A;Reference number: A60521; MUID:9027907; PMID:2109669
A;Accession: A60521
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A,Residues: 1-5 <BON>
(S.Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase, hexosyltransferase, phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experi
C;Accession: A32039
R;Horvath, A.; Kastin, A.J.
J; Biol. Chem. 264, 2175-2179, 1989
J; Biol. Chem. 264, 2175-2179, 1989
J; Lite: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor A;Reference number: A32039; MUID:89123285; PMID:2563371
A;Reference rumber: A32039
A;Residues: 1-4 cHOR>
A;Residues: 1-4 cHOR>
A;Residues: 1-4 cHOR>
A;Residues: 1-4 cHOR>
A;Reverimental source: brain
C;Reywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
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N,Alternate names: glycogen phosphorylase b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 28.9%; Score 11; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 2.86+05; Matches 2; Conservative 0; Mismatches 0; Indels
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28.9%; Score 11; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          schwannomin - mouse (fragment)
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R;KO, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Amm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Ritle: Genetic mapping of 40 wIUD:94319082; PMID:8043949
                                                          C;Accession: E60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A;Title: Isolation and partial characterization of major protein antigens in the culture A;Reference number: A60274; MUID:9109989; PMID:1898899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R-phycocrythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment) C;Species: Gastroclonium coulteri C;Species: Gastroclonium coulteri C;Date: 07-Mar-1988 #text_change 23-Mar-1993 C;Accession: F22565 Farlorz, A.V.; Glazer, A.N. J. Hotz, A.V.; Glazer, A.N. J. Hotz, Cham. 260, 4856-4863, 1885 A;Title: Characterization of the bilin attachment sites in R-phycocrythrin. A;Reference number: A22565; MUID:85182601; PMID:3886644 A;Accession: F22565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin B1 - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: 149421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DMA
A;Residues: 1-6 <RES>
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829
                          C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
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Best Local Similarity 100.0%; Pred. No. 2.88+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>
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C;Accession: IS1049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Brille: J. Stanctural and functional analysis of the rainbow trout (Oncorhyncus mykiss) m A;Reference number: IS1049; MUID:95324545; PMID:7601121
A;Accession: IS1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: S43959
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Nucleic Acids Res. 22, 1389-1393, 1994
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A;Reference number: S43956; MUID:94248036; PMID:8190629
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                                                                                                                                                                                                                                                      R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C;Species: Gastroclonium coulteri
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: X80181; NID: 91019799; PIDN: CAA56466.1; PID: 94379328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Oncorhynchus mykiss (rainbow trout)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                            C;Accession: A22565
R;KIOCZ, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A22565; MUID:85182601; PMID:3886644
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C.Species: Homo sapiens (man)
C.Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
                                              Gaps
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               Pred. No. 2.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.7%; Score 9; DB 3; Length 3; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 1; Conservative 0; Mismatches 0; Indels
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            50.0%;
                                         Conservative
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C, Keywords: immunoglobulin
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            Similarity
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                                                                                                                                     C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C;Accession: 137263
R;Wabebr, G: Habener, J.F.
Bndocrinology 131, 2010-2015, 1992
A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna A;Accession: 137263; MUID:93010691; PMID:1396344
A;Accession: 137263
A;Status: preliminary; translated from GB/EWBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              917-Oprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C'Species: Bos primigenius taurus (cattle)
C'Species: Bos primigenius taurus (cattle)
C'Accession: H48394
R'Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
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C.Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C.Accession: C22565
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J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
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                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-6 <RES>
A;Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C;Genetics:
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Pred. No. 2.8e+05;
0; Mismatches 1; Indels
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A;Residues: 1-6 <MAI>
A;Residues: 1-6 <MAI>
A;Rxperimental source: milk
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A48394; MUID: 93250576; PMID: 8485470
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Matches 2; Conserv
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Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1
Db 2 C 2

RESULT 15

S55238
pallidipin - assassin bug (fragment)
C; Species: Triatoma pallidipennis (assassin bug)
C; Species: Triatoma pallidipennis
C; Species: Triat
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March 8, 2004, 12:31:54; Search time 10 Seconds (without alignments) 31.242 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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38
1 CVPLTC 6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:*

Database :

	Description	P82096 litoria mih	hermen	litoria	mytiliia	mytilus	periplar		٠	P19916 pseudomonas	P36515 gaccharomyc		citro					P42985 leptinotars		-		P82073 litoria rub	P81351 clostridium	P02731 homo sapien	P42562 hirudo medi		P58707 anthopleura	P81817 carcinus ma	litoria	P54714 canis famil	P80628 zea mays (m		4272	P58706 anthopleura
SUMMARIES	QI .	EIO1 LITRU	VP19 HSV1K	EI03 LITRU	CIP1 MYTED	CIP2 MYTED	PRCT PERAM	TRPI_PSEPU	THYL_PIG	DCML_PSECH	RM01_YEAST	TUFT HUMAN	BIOA_CITFR	BPP7_BOTIN			SUGA_ACHDO		TMOF_SARBU					EOSI HUMAN		FLRF_HIRME		AL14_CARMA		TPIS_CANFA		ACPH_RABIT	- 1	FYRI_ANTEL
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SECURINE FROM N.A.
MEDLINE-91101287; PubMed=1646198;
Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
Silverstein S., Wagner E.K.;
"Analysis of the herpes simplex virus type I promoter controlling the

Herpes simplex virus (type 1 / strain KOS). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus. NCBI_TAXID=10306;

P232I0, 01-NOV-1991 (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update) Cappid assembly and DNA maturation protein (Virion protein UL38) (Capsid protein VP19C) (Fragment).

P41853 artioposthi P82071 litoria rub P82673 mus musculu P19918 pseudomonas P42563 hirudo medi P01162 macrocallis P12997 citrobacter P58649 octopus min P38005 chlamydia t P41491 locusta mig P01157 homo sapien P35904 achatina fu			orata; Buteleostomi; Oidea; Hylidae;	Wallace J.C.; Australian buzzing tree frog skin peptides from Litoria	⟨८64,	Length 6; 5; 0; Indels 0; Gaps 0;	
5 1 FARP ANTTR 5 1 RE21_LITRU 5 1 UF01_MOUSE 4 1 DCMS_PECH 4 1 FAR4_HIRME 4 1 FORF MACNI 5 1 BIOB_CITFR 5 1 UXA4_CHLTR 6 1 LOKALCOMI 6 1 LOKALCOMI 8 1 ACH1_ACHFUR	ALIGNMENTS TO, BRI; 6 AA.	Created) Last sequence update) Last annotation update)	Discutin 1. Discutin to the fired frog). Bikaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Battachia; Antra; Neobatrachia; Hyloidea; Redofryadinae; Litoria.	Tyler M.J., lands of the son with the	hem. 52:639-645(1999). LULAR LOCATION: Secreted. SPECIFICITY: Skin. defense peptide; Amidation. 6	34.2%; Score 13; DB 1; 66.7%; Pred. No. 1.4e+05 ive 1; Mismatches	
34 335 336 336 337 338 339 339 344 447 11 1 2 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		28-FRB-2003 (Rel. 41, 28-FRB-2003 (Rel. 41, 10-OCT-2003 (Rel. 42,	Jacotin 1. Litoria rubella (Desert tree frog) Enkaryota, Metazoa; Chordata; Cran Amphibia; Batrachia; Anura; Neobat Pelodryadinae; Litoria. NCBI_TaxID=104895;	tin secret 2.A., Bowi 3 from the ectrica.	Aust. J. Chem. 52:639-645(1999)!- SUBCELLULAR LOCATION: Secreted -!- TISSUE SPECIFICITY: Skin. Amphibian defense peptide; Amidati MOD RES 6 6 AMIDA SEQUENCE 6 AA; 792 MW; 6683704	Query Match Best Local Similarity 66. Matches 2; Conservative	2 VPL 4 : 2 VPI 4
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Gaps

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TISSUE-Pedal ganglion, MEDLINE-88240357; PubMed=3377776; MEDLINE-88240357; PubMed=3377776; MEDLINE-88240357; PubMed=3377776; Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.; Structures and actions Of Whilus inhibitory peptides."; Biochem. Biophys. Res. Commun. 123:1376-1382(1988).
--- FUNCTION: Inhibitory action on contractions in several molluscan
       Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBL_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mytilus edulis (Blue mussel).
Bukaryota, Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TAXID=6550;
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Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
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01-0AN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Contraction-inhibiting peptide II (MIP II)
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(Rel. 01, Last sequence update)
(Rel. 31, Last annotation update)
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50.0%;
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50.0%;
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Hormone; Amidation.
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Matches 1; Conserv
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21-JUL-1986
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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expression of UL38, a true late gene involved in capsid assembly."; J. Virol. 65:769-786 (1991).
-!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBREDED. BINDS DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Skin secretion, Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Literi electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
NCBI_TAXID=104895;
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                                                                                     -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
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SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

        MOD_RES
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        AMIDATION,

        SEQUENCE
        5 AA; 630 MW; 668761F2C9A00000 CRC64;

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01-0AN-1990 (Rel. 13, Last sequence update)
12-DEC-1998 (Rel. 37, Last annotation update)
Contraction-inhibiting peptide I (MIP I).
Mytilus edulis (Blue mussel).
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Capsid assembly; Coat protein; DNA-binding.
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
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28-FEB-2003 (Rel. 41, Last sequ
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ID CIP1_MYTED
AC P13736;
DT 01-JAN-1990
DT 01-JAN-1990
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DE CONTRACTION-
OS MYTILUS EGUI
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P01151;
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                                                                                                        Starratt A.N., Brown B.E.; "Structure of the pentapeptide proctolin, a proposed neurotransmitter
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15-MAR-2004 (Rel. 43, Last annotation update)
HTH-type transcriptional regulator trpl (TrpBA operon transcriptional
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MEDIME=6623789; PubMed=2872661;
Stangier J., Dircksen H., Keller R.;
Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.",
Pepticolices 7:67-72(1986).
-!- FUNCTION: Stimulates cardiac output and hindgut motility,
modulates visceral and skeletal muscle in many arthropods.
-!- TISSUB SPECIFICITY: Found in the lateral white neurons and in
                                                                                                                                                                                         MEDLINE-81225865; PubMed-6113690; O'Shea M., Adams M.E.; "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                               Shabanowitz J., "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Carcinus maenas (Common shore crab) (Green crab).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
                                                                                                                                                                                                                                                                SPECIES=L.polyphemus;
MEDLINE=90287800; PubMed=2356151;
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.1%; Score 8; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05; ive 1; Mismatches 0; Indels
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01-JUN-1994 (Rel. 29, Last seq
15-MAR-2004 (Rel. 43, Last ann
                                                                              SPECIES=P.americana;
MEDLINE=76074708; PubMed=576;
                                                                                                                                             Life Sci. 17:1253-1256(1975).
                                 Blattidae, Periplaneta.
NCBI TaxID=6978, 6850, 6759;
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                                                                                                                                                                                 SPECIES=P.americana;
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SEQUENCE FROM N.A.
STRAIN=PPG1 C1S;
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Matches 1; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide.
SEQUENCE 5
                                                                                                                                 insects.
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                                                                     SECUENCE
                                                                                                                                                                                                                                                       SEOUENCE
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TRPI PSEPU
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDILES-7039904; PubMed=4982117;
Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
The identity of chemical and hormonal properties of the thyrotropin releasing hormone and pyroglutamy1-histidy1-proline amide.";
Biochem. Biophys. Res. Commun. 37:705-710(1969).
                                                                                                                                                      -1-FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNTS. IN THE ABSENCE OF THE INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
-1- SIMILARITY: Contains 1 HTH 1yer-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Notophthalmus viridescens (Bastern newt) (Triturus viridescens). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus. NCBL_TaxID=9823, 9940, 8346, 8316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Thyrollberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-Sheep, TISSUE-Hypothalamus,
Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
Eberly L., Crawford I.P.,
"DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro, IPR000847; HTH LyGR.
PROSITE: PSSO931; HTH LYSR; PARTIAL.
Tryptophan biosynthesis; Transcription regulation; Activator;
DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-Pig; IISSUE-Hypothalamus;
MEDLINE-70136150; PubMed-4944938;
Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
"Structure of porcine thyrotropin releasing hormone.";
Bjochemistry 9:1103-1106(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig),
Ovis aries (Sheep),
Bombina orientalis (Oriental fire-bellied toad), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON TER 6 8 SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 8; DB 1; Le
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 AA.
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X13299; CAA31660.1; -.
                                                                                                                          Biochimie 71:521-531(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Conservative
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MEDLINE=91285106; PubMed=2060626;
Grobmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.,
Kitakawa M.;
-! - SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.";
PEBS Lett. 284:51-56(1991).
PIR; S17255; S17255.
SGD; L0002681; MRPL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.; "The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butherla, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                    0; Indels
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100.0%; Pred. No. 1.4e+05;
tive 0; Mismatches 0; Indels
                                                                                                                                   DB 1; Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON TER 4 4 SEQUENCE 4 AA, 402 MW; 7771B2D5D000000 CRC64;
                                                                                         SEQUENCE 4 AA; 441 MW; 7761E876F000000 CRC64;
                                                                                                                                                    1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-CCT-2001 (Rel. 40, Last amnotation update)
Phagocytosis-stimulating peptide (Tuftsin)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 AA.
                                                                                                                                                                                                                                                                                                                                             4 AA.
                                                                                                                               18.4%; Score 7; DB 1
100.0%; Pred. No. 1.4
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosomal protein; Mitochondrion.
                                     PIR; PL0140; PL0140.
Oxidoreductase; Molybdenum.
                                                                                                                                                    Best Local Similarity 100.0
Matches 1; Conservative
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IMMUNOGLOBULIN CLASS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
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P-5-4
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P01858;
                                                                                                                                                                                                                                                                                                                                           RM01 YEAST
P36515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                    Query Match
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TUFT HUMAN
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Matches
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-!- FUNYION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/ neuromodulator in the central and peripheral nervous systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE=90055678; PubMed=2818128;
Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
-!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
                                                                                                                                                                                                                                                                                                                                                                             SPECIES-N.viridescens;
MEDLINE=15035605; PubMed=4214528;
Grimm-Joergensen Y., McKelvy J.F.;
"Blosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
J. Neurochem. 23:471-478 (1974).
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01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUTL.
Pseudomonas carboxydohydrogena.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                SPECIES-B.orientalis; TISSUE-Skin; MEDLINE-76138399; PubMed=815011; Yasuhara T., Nakajima T. Makajima T. Tetrario Courrence of Pyr-His-Pro-NH2 in the frog skin."; Chem. Pharm. Bull. 23:3301-3303(1975).
                                                                                                   MEDLINE-70163386; Pubmed=4985794;
Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amidation; Pyrrolidone carboxylic acid.

MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

MOD RES 3 3 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                          Guillemin R.; "Characterization of ovine hypothalamic hypophysiotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.4%; Score 7; DB 1; Length 3; 100.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 AA; 380 MW; 7761F6B00000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AA.
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-!- COFACTOR: Molybdenum (molybdopterin).
       spectrometry.";
Org. Mass Spectrom. 5:221-228(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Conservative
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                                                                                                                                                                                                Nature 226:321-325(1970).
                                                                                                                                                                                  TSH-releasing factor."
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PIR; A92971; A92971.
PIR; A93750; RHSHT.
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                                                                                     SPECIES=Sheep;
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P19916;
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SEQUENCE
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                                                                 SYNTHESIS
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MEDLINE-90331557; PubMed=2186615;

A Cintra A.C.O., Vieira C.A., Giglio J.R.,

B Cintra A.C.O., Vieira C.A., Giglio J.R.,

B Cintra A.C.O., Vieira C.A., Giglio J.R.,

B Peptides from Bothrops insularis snake venom.",

C -1 FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.

C Lacts as an indirect hypotensive agent.

DR PIR, G13196, G37196, G37196.

Hypotensive agent; Pyrrolidone carboxylic acid.

MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

SEQÜENCE 5 AA, 629 MW, 776DC37326B00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994. (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bradykinin-potentiating peptide S5,2 (SA) (Angiotensin-converting enzyme inhibitor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Skin secretion; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Mabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bothrops insularis (Island jararaca) (Queimada jararaca).
Bukaryota, Metazoa; Chorddta; Craniata, Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Litoria rubella (Desert tree frog).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachla, Annra, Neobatrachia, Hyloidea, Hylidae; Pelodryadines, Litoria.

NCBL_TaxID=104895;
                                    Score 7; DB 1; Length 5;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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nes 0; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                  5 AA.
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100.0%; Pred. No. 1.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                  PRT;
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Skin.
                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-FEB-1994 (Rel. 28, Last seq
                                    18.4%;
illarity 50.0%;
Conservative
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                               Query Match
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P30425;
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P82100;
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EI04_LITRU
                                                                                   Matches
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               Fidalgo B.V., Najjar V.A.;
"The physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";
Biochemistry 6:3386-3392(1967).

-I MISCELLANEOUS: An IgG (called leucokinin) binds reversibly to the
                                                                                                                                                                  cell membrane of neutrophils in the blood. Leucokininase on the membrane releases the active peptide tuftsin from the gamma chain. Tuftsin is essential for maximum stimulation of the phagocytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=89006280; PubMed=2971595;
Shiuan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
"Irranscriptional regulation and Salmonella typhimurium biotin operons.";
Citrobacter freundii and Salmonella typhimurium biotin operons.";
Gene 67:203-211(1988).
:- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- COPACTOR: Pyridoxal phosphate.
-!- PATHWAY: Biotin biosynthesis.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine 8-amino-7-oxonomanoate aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 4;
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PROSITE; PS00600; AA TRANSPER CLASS 3; PARTIAL.
Biotin biosynthesis; Transferase; Aminotransferase;
                                                                                                                                                                                                                                                                                                                  GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006909; P:phagocytosis; NAS.
SEQUENCE 4 AA; 501 NW; 74176321C000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Score 7; DB 1
100.0%; Pred. No. 1.4.
tive 0; Mismatches
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PIR; 140697; 140697.
MEDLINE=68091045; PubMed=4169272;
                                                                                                                                                                                                                                      activity of neutrophile.
PIR; A02147; A02147.
MIM; 191150; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Conservative
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Best Local Similarity
Matches 1; Conserv
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Gaps

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PEQUENCE.

***REDLINE=87057369; PubMed=3782138; ABCINESKINE=87057369; PubMed=3782138;

***MEDLINE=87057369; PubMed=3782138;

***ARITION N.** Loow L.M.*;

***Indication and pore-forming activity of two hydrophobic more managed by the secretion of the Red sea moses sole (Pardachirus RT polypeptides from the secretion of the Red sea moses sole (Pardachirus RT marmoratus).";

***ARITION Exhibits unusual shark repellent and surfactant properties. Forms voltage-dependent, ion-permeable channels in membranes. At high concentration causes cell membrane lysis.

**C --- SUBGRIGHTR Monomer. In aqueous solution exists as a tetramer.

**C --- SUBGRIGHTR Secreted.

**C --- SIMILARITY: Belongs to the pardaxin family.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Pardaxin II (PXII) (Fragment).
Pardachirus marmoratus (Red sea moses sole).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinoperygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Soleoidei, Soleidae; Pardachirus.
NCBI_TAXID=31087;
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                                                                                                                                           Score 7; DB 1; Length 5;
Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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NON TER 5 5
SEQUENCE 5 AA, 614 MW, 7769C9C8100000 CRC64;
Amphibian defense peptide; Amidation.

MOD RES 5 AMIDATION.

SRQUENCE 5 AA; 616 MW; 61F2D1A059A00000 CRC64;
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Best Local Similarity 50.0%;
Matches 1; Conservative 1
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Matches 1; Conserv
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PARZA
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Search completed: March 8, 2004, 12:37:29
Job time : 11 secs

5 P S

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RESULT 1

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 8, 2004, 12:34:59 ; Search time 39 Seconds
(without alignments)
48.541 Million cell updates/sec

US-09-761-636A-12 Perfect score:

Scoring table:

1 CVPLTC 6

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1017041 segs, 315518202 residues Searched:

11 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 6

Post-processing: Minimum Match 0* Maximum Match 100* Listing first 45 summaries

Database :

SPTREMBL_25:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_human:*
5: sp_nammal:*
5: sp_mammal:*
5: sp_organelle:*
5: pp_phage:*
5: sr_l=*
5: pp_phage:*
5: sr_l=*
5 sp_vertebrate:*
sp_unclassified:* sp_plant: *
sp_rodent: *
sp_virus: * rvirus:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

sp archeap:*

SUMMARIES

		Description	Lien pulled BB330B	DRATEG BETTE OFFICE	P83073 bacillus ce	P83533 lactobacill	P82181 gninacia	D82541 animacia ol	P82182 spinacia ol	P83568 Renia offic	O00423 #3### OFFIC	000007 hordon 20.	P83570 sepia offic) (
		ID	P83308	P83569	P83073	P83533	P82181	P82541	P82182	P83568	008433	00000	P83570	
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		e Match Length DB I	5	9	ß	9	9	9	9	4	4	L.	7	
de	Query	Match	31.6	23.7	13.2	13.2	13.2	13.2	13.2	10.5	10.5	5.3	0.0	
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	Result	No.	-	7	m	4	ហ	9	7	89	σ	10	11	

Zatylny C., Marvin L., Gagnon J., Henry J.;

#Pertilization in Sepia officinalis: the first mollusk spermattracting peptide.";

Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).

-I- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
COLLISION.

-I- DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES FURING
VITELICGENESIS. ACCIMULATES IN THE OCCTTES BEFORE BEING SECRETED
DUNING FERTILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED OCCTTE.
ACCUMULANES IN THE BGG CAPSULE AFTER FERTILIZATION.

-I- MASS SPECTROMETRY: MM-596.6; METHOD=MALDI. FMRFamide-like neuropeptide (LPLRF-amide).
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae, PubMed=613771;
Docktag, G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
A novel active pentapeptide from chicken brain identified by
antibodies to FMRFamide."; Gaps 01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
61-UUN-2003 (TrEMBLrel. 24, Last sequence update)
Sperm attracting peptide SepSAP,
Sepia officinalis (Common cuttlefish).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiiae, Sepia. NATURE 305:328-330(1983).' -!- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR. -!- SIMILARITY: BELONGS TO THE FARP (FMRRAMIDE RELATED PEPTIDE) [1] -SRQUENCE, FUNCTION, DEVELOPMENTAL STAGE, MASS SPECTROMETRY, AND .; 0 Score 12; DB 13; Length 5; Pred. No. 1e+06; 1; Mismatches 0; Indels Length 6; GO; GO:0007218; P:neuropeptide signaling pathway; TAS. Last sequence update) AMIDATION. 69D4073767400000 CRC64; 6 6 AMIDATION. 6 AA; 597 MW; 72CB676AA0470000 CRC64; 23.7%; Score 9; DB 5; 50.0%; Pred. No. 1e+06; tive 1; Mismatches 5 A.A. 6 AA. Created) PRT; 31.6%; 66.7%; 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2003 (TrEMBLrel. 24, Query Match Best Local Similarity 50.07, SEQUENCE 5 AA; 645 MW; Neuropeptide; Amidation. MOD_RES 5 5 2; Conservative PRELIMINARY; PRELIMINARY; SEQUENCE, AND SYNTHESIS. Query Match Best Local Similarity NCBI_TaxID=9031; TISSUE=Egg; PubMed=12207899; NCBI_TaxID=6610; :---1 LPL 3 2 VPL 4 TISSUE=Brain; Amidation. MOD RES SEQUENCE P83308; P83569 P83569; P83308 Gallus Matches RESULT 2 P83569 ଚ 셤

0

ALIGNMENTS

0

Gaps

; 0

0; Indels

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STAIN—CV. ALWARO; TISSUE=Leaf;

X Yamaguchi K., Subramanian A.R.;

Yamaguchi K., Subramanian A.R.;

The plastid ribosomal proteins. Identification of all the proteins in the 50 S subunit of an organelle ribosome (chloroplast).";

J. Biol. Chem. 275:28466-24482[2000).

J. Biol. Chem. 275:28466-24482[2000).

C. -- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 238 RIBOSOMAL RNA.

-- SUBCRLIGIAR LOCATION: GLADOROPLAST.

-- STRINGS SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

--- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

--- SINILARITY: BELONGS TO THE LIOP FAMILY OF RIBOSOWAL PROTEINS.

GO; GO:00199431 F: FRAM binding; IEA.

GO; GO:00199431 F: RIBOSOMAL LIOP PRATILY of Tibosome; IEA.

InterPro; IPRO02363; Ribosomal LiDeub.

PROSITE: PSOINGS RIBOSOMAL LIOP PRATILY.

--- SINILARITY: PSOINGS RIBOSOMAL LIOP PRATILY.

INTERPRESSIES PROTEINS RIPOSOMAL LIOPATION.

PROSITE: PSOINGS RIPOSOMAL LIOPATION.
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RE STRAIN=CV. ALWARO; TISSUE=Leaf;

REALIN=CV. ALWARO; TISSUE=Leaf;

REALINECV. ALWARO; TISSUE=Leaf;

REALINECV. ALWARO; TISSUE=Leaf;

RAMEQUCHI K., von Knoblauch K., Subramanian A.R.;

RT "The plastid ribosomal proteins. Identification of all the proteins in real subunit of an organelle ribosome (chloroplast).";

The plastid ribosomal proteins. Identification of all the proteins in RL or Biol. Chem. 37:20455-20465(2000).

C. BIOL. Chem. 37:20455-20465(2000).

C. FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA...

C. FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA...

C. I- RASS SPECTROMETRY: NM=10477.0; METHOD=ELECTROSPRAY...

C. I- MASS SPECTROMETRY: M=10495; METHOD=ELECTROSPRAY...

C. I- MASS SPECTROMETRY: M=10495; METHOD=MALDI...

C. I- MASS SPECTROMETRY: M=10495; METHOD=MALDI...

C. I- MISCELLANGOUS: ON THE 2D-GEL ITS NM IS: 12 KDA...

C. I- MISCELLANGOUS: ON THE 2D-GEL ITS NM IS: 12 KDA...

C. I- SIMILARITY: BELONGS TO THE 519P FAMILY OF RIBOSOWAL PROTEINS.

CO: GO: GO: GO: 00019643; F: RNA binding; IEA...

DR GO: GO: 0019643; F: RNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Colloroplast So ribosomal protein L10 beta (Fragment).
Spinacia oleracea (Spinach).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllalee; Amaranthaceae; Spinacia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TEMBLrel. 15, Created)
01-OCT-2000 (TEMBLrel. 15, Last sequence update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Chloroplast 308 ribosomal protein S19 beta (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA; 675 MW; 6321B415B05DB000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosomal protein; Chloroplast; rRNA-binding.
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Chloroplast.
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Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
Bacteria, Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBL_TaxID=1625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 13.2%; Score 5; DB 2; Length 5; Local Similarity 100.0%; Pred. No. 1e+06; Osesvative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1e+06;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     88 kDa protein (Fragment).
Bacillus corens.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1396;
                                                                                                                                                                                                                                                    01-0CT-2001 (TEMBLrel. 18, Created)
01-0CT-2001 (TEMBLrel. 18, Last sequence update)
01-0CT-2003 (TEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 5 AA; 623 MW; 6B01AAA336F00000 CRC64;
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Browne N., Dowds B.C.A.;
Submitted (JUL-2001) to Swiss-Prot.
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Matches 1; Conservative
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01-JUN-2003 (TrEMBLrel.
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STRAIN=DSM 20451;
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Zarylny C., Gagnon J., Boucaud-Camou E., Henry J.;
"ILME: a waterborne pheromonal peptide released by the eggs of Sepia
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                      STRAIN-Gunn,
MEDLINE-91282758; PubMed=1840486;
MEDLINE-91282758; PubMed=1840486;
MEDLINE-91282758; Rolwai O.;
Medetic defect of bilirubin UDP-glucuronosyltransferase in the hyperbilirubinemic Gunn rat.";
Blochem. Blophys. Res. Commun. 177:1161-1164(1991).
BMBL; S38636; AAB19259.1;
GO: GO:0016740; F:transferase activity; IEA.
               SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
                                                                                                                                                                                                                                                                                                                                                                     10.5%; Score 4; DB 5; Length 4; 100.0%; Pred. No. 1e+06; ative 0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                                                                                                                                                         4 AA; 505 MW; 6B1697203000000 CRC64;
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SEQÜENCE 4 AA; 473 MW; 633732C42000000 CRC64;
                                                                                                                Biochem. Biophys. Res. Commun. 275:217-222(2000)
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01-NOV-1996 (TrEMBLrel. 01, Created)
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                                         TISSUE=Egg;
PubMed=10944467;
                                                                                                                                                            TISSUE=Egg;
PubMed=12207899;
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A Yamaguchi K., Subramanian A.R.;

AT Yamaguchi K., Subramanian A.R.;

AT The plastid ribosomal proteins Identification of all the proteins in the 50 S aubunit of an organelle ribosome (chloroplast).";

L. 50 S aubunit of an organelle ribosome (chloroplast).";

L. 51 J. 8101. Chem. 275:28466-28482(2000).

C. --- FUNCTION: THIS PROTEIN BINNE DIRECTLY TO 23S RIBOSOMAL RNA.

C. --- STRUELLUTAR LOCATION: CHLOROPLAST.

C. --- STRUELLUTAR SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.

C. --- STRUILARITY: BELONGS TO THE LIDP FAMILY OF RIBOSOMAL PROTEINS.

C. --- STRUILARITY: BELONGS TO THE LIDP FAMILY OF RIBOSOMAL PROTEINS.

C. --- STRUILARITY: BELONGS TO THE LIDP FAMILY OF RIBOSOMAL PROTEINS.

CO. GO:0009507; C:chloroplast; IEA.

DR GO; GO:0019735; F:structural constituent of ribosome; IEA.

BROSITE; PSO1109; RIBOSOMAL LIŌ: PARTIAL.

KW RIDOSOMAL PROTEIN: Chloroplast; FRNA-binding.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Spinacia.
NCBI_TaxID=3562;
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Decapodiformes; Sepioidea; Sepiidae; Sepia.
NCBI_TaxID=6610;
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GO; GO:0003735; F:structural constituent of ribosome; IRA.
                                                                                                    / Match 13.2%; Score 5; DB 10; Length 6; Local Similarity 100.0%; Pred. No. 1e+06; les 1; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                            01-JUN-2000 (TrEMBLrel. 14, Created)
01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Chloroplast 50S ribosomal protein L10 gamma (Fragment).
                                                                       6 AA; 732 MW; 63333735A411C000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA; 675 MW; 6321B415B05DB000 CRC64;
                  InterPro; IPR00222; Ribosomal 819.
PROSITE; PS00323; RIBOSOWAL S19; PARTIAL.
Ribosomal protein; Chloroplast; rRNA-binding.
NON TER
SEQÜENCE 6 AA; 732 MW; 63333735A411C000 C1
                                                                                                                                                                                                                                                                          e AA
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Sepia officinalis (Common cuttlefish)
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Henry J. Favral P., Boucaud-Camou E.;

"Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related peptide inhibiting the motility of the mature oviduct in the cutilefish, Sepia officianlis.";

Peptides 18:1469-1474(1997).

-!- FUNCTION: REGILARORY NEUROBEPTIDE WITH MYOTROPIC ACTIVITY

TARGETING THE DISTAL OVIDUCT. INHIBITS THE MOTILITY OF THE OVIDUCT BY DECREABING TONIS, PREQUENCY AND AMPLITUDE OF CONTRACTIONS.

-!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI.

GO, GO:0007218; P:neuropeptide signaling pathway; IEA.

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Sepia officinalis (Common cuttlefish).
Bukaryota, Metazoa; Nollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Bocapodiformes, Sepioidea; Sepiidae; Sepia.
                                                              Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                              MEDINE-91329704; PubMed=1831055;
Jacobsen J.V., Close T.J.;
Jacobsen J.V., Close T.J.;
"Control of transient expression of chimaeric genes by gibberellic acid and abscistc acid in protoplasts prepared from mature bareley aleurone layers.";
Plant Mol. Biol. 16:713-721(1991).
EMBL; X54643; CAA38455.1;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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2 AA; 261 MW; 737810000000000 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2003 (TrEMBLrel. 23, Alpha amylase (Fragment).
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Best Local Similarity
Matches 0; Conserv
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PubMed=9437704;
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SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=4513;
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1 CVPLTC 6
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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	Description	Aano4531 VRCB hase					_																Aar08270 Destide 1		Aave 6012 Dentide f	, N	
SUMMARIES	di	AAU04531	AAY61488	AAY62223	AAY62763	AAY62006	AAY64259	AAY85373	AAY62757	AAY62488	AAY44431	AAR15772	AAR49769	AAR77833	AAW04459	AAW67428	AAW31456	AAY63235	AAY61927	AAY62132	AAY63263	AAR51652	AAR08270	AAR78749	AAY69213	AAY56095	
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t 1	No.	Н	7	Э	4	ഗ	9	7	∞	on ·	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25	

Aay68185 Haemoglob Aag78351 Haemoglob				Aaw08703 Honeybee	Aar95842 IGF-1 mut	Aaw11026 Immunomod		Aaw51950 Pentide h		-	Aab23802 Phage dis	Aav61733 Cadherin-	Aab31387 Peptide w	Abb46600 Desmocoll			,
5 3 AAY68185 5 4 AAG78351	5 5 ABB83467 5 5 AAO17897	5 5 ABB77196	5 5 ABB77197	6 2 AAW08703	6 2 AAR95842	6 2 AAW11026	6 2 AAW44954	6 2 AAW51950	6 2 AAY09380	6 2 AAW89219	6 3 AAB23802	6 3 AAY61733	6 4 AAB31387	6 5 ABB46600	6 5 ABB46920	4 2 AAW43270	5 2 AAY29743
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ALIGNMENTS

RESI AAU	RESULT 1 AAU04531 LD AAU04531 standard; peptide; 6 AA.
\$ \$ \$	AAU04531;
1	26-SEP-2001 (first entry)
(日)	VEGF based monocyclic peptide 9.
*****	Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rhematoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
88	Synthetic.
\$E	Key Location/Qualifiers Disulfide-bond 16 /note= "This bond cyclises the peptide"
E E	WO200152875-A1.
1	26-JUL-2001.
\$ # \$	18-JAN-2001; 2001MO-US001533.
1 H H	18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.
\$ 8 \$	(LUDW-) LUDWIG INST CANCER RES.
4 E 3	Achen MG, Hughes RA, Stacker S, Cendron A;
4 倍;	WPL; 2001-442248/47.
\$ # # # # # # # # # # # # # # # # # # #	Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
S X	Claim 49; Page 32; 102pp; English.
888888	The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

WPI; 2000-038791/03.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, condition acid deleted prior to cyclisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis in neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, recondition is diabetic retinopathy, psoriasis, arthropathy, creprovascular accident, post-engloplasty restenosis, head heat or cold trauma, substance-induced neovascularisation of the liver, excessive creprovascular accident, post-engloplasty restenosis, head, heat or cold trauma, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability or brain. The peptides are used to induced by vEGF. Or brain. The peptides are used to induced by vEGF. Or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by vEGF. VEGF. Or -D and are also used in combination with an anti-inflammatory agent, to treat a discussion in the perior or present and anti-inflammatory agent, to treat a discussion in the perior or present and anti-inflammatory agent to treat a discussion or present and processed and anti-inflammatory and and architectures and and anti-inflammatory and architectures and and anti-inflammatory and architectures and and anti-inflammatory and and anti-inflammatory and and anti-inflammatory and and anti-inflammatory and anti-inflammat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy
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Best Local Similarity
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20-JAN-1999;
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Matches
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The present invention describes cadherin modulating agents (MA)

comprising peptides which comprise a nonclassical cadherin cell adhesion

comprising peptides which comprise a nonclassical cadhering

cecognition (CAR) sequence. The MAs can be used for modulating

nonclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal,

can manal, inhibiting metastasis of a cancer in a mammal, inhibiting

a maiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-

expressing cell, preventing or treating obesity in a mammal, stimulating

blood vessel regression in a mammal, enhancing delivery to the

central nervous system, treating a demyelinating neurological disease,

increasing vasopermeability in a mammal. Enhancing adhesion of

nonclassical cadherin-expressing cells, inhibiting synaptic stability in

a mammal, or preventing pregnancy in a mammal. They can also be used for

c.g. enhancing or directing neurite outgrowth, facilitating wound healing

or reducing scar tissue, or enhancing adhesion of foreign tissue in a

mammal. They can also be used for treating e.g. psoriasis, arthritis, age

related macular degeneration, multiple sclerosis and diabetes. The

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                                                               New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
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Pred. No. 1.4e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention
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                                                                                                                                                                      Claim 36; Page 172; 252pp; English.
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66.7%;
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Location/Qualifiers

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Gour BJ, Byers S;

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98US-00073040. 98US-00187859. 99US-00234395. 99US-00264516.

99WO-CA000363.

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New cadherin modulating agents, used for modulating nonclassical cadherin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 72; Page 193; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ADHE-) ADHEREX TECHNOLOGIES INC.
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                                                                                                    Disulfide-bond
                              Homo sapiens.
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20-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion cereognition (GAR) sequence. The MAS can be used for modulating nonclassical cadherin—mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the Skin of a mammal, enhancing delivery of a drug though the Skin of a mammal, and mammal inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cells, preventing or treating obesity in a mammal, stimulating carpression in a mammal, enhancing delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal. They can also be used for conclassical cadherin—expressing cells, inhibiting synaptic stability in a mammal. They can also be used for treating e.g. psoriasis, and in bioreactors.

Any of the can also be used for treating e.g. psoriasis, and in bioreactors. Any of the conclassical and adhesion and diagnosis and in bioreactors. Any of the conclassical and Any 13188 represent sequences used in the conclassical and any of the conclassical cadherin—expressing mammal. They can also be used for detection and diagnosis and in bioreactors. Any of the conclassical the conclassical cadherine specifically claimed peptides, and cadherine specifically claimed peptides and cadherine cadherine cadherine cadherine cadherine cadherine cadherine cadherin
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                                                                                                                                                                                                                                                                                                                                           New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 54; Page 184; 252pp; English.
                                                                                                                                                                                    (ADHE-) ADHEREX TECHNOLOGIES INC.
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                                                                                                                                                                                                                                    Gour BJ, Byers S;
                                                                                                                                99US-00264516.
99WO-CA000363.
                                                    98US-00073040.
                                                                           98US-00187859.
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  05-MAY-1999;
                                                  05-MAY-1998;
                                                                           06-NOV-1998;
20-JAN-1999;
                                                                                                                                38-MAR-1999;
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The present invention describes cadherin modulating agents (MA)

Comprising peptides which comprise a nonclassical cadherin cell adhesion

comprising peptides which comprise a nonclassical cadherin cell adhesion

comprision (CAS) sequence. The MAS can be used for engine in the conclassical cadherin-mediated functions. They can be used for e.g.

Inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a trung through the skin of a mammal, challing metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a mammal, inhibiting confersion of the capression in a mammal, enhancing delivery to the capression in a mammal, enhancing delivery to the contral nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal. They can also be used for a mammal. They can also be used for treating e.g. psoriasis, arthritis, age creducing sear tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age creducing sear tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age creducing sear tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for detection and diagnosis and in bioreactors.

ANG6552 to ANG6552 represent specifically claimed peptides, and the ANG851181 to ANG6552 and diagnosis and in bioreactors.

ANG6552 to ANG6653 to ANG6552 represent specifically claimed peptides, and the ANG8550 to ANG6550 the ANG6550 to ANG6550 the ANG6550 to ANG6550 to ANG6550 the ANG6550 to ANG6550 the ANG6550 to ANG6550 the ANG6550 to ANG6550 the A
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Pred. No. 1.4e+06;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the exemplification of the present invention
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Best Local Similarity
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WO9957149-A2.
       Homo sapiens.
            11-NOV-1999
       Synthetic.
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AAY64259
RESULT
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Comprising Peptides which comprise a nonclassical cadherin cell adhesion

comprising Peptides which comprise a nonclassical cadhering expension (CRR) sequence. The MAS can be used for e.g.

comprising adhesion of nonclassical-cadherin expressing cells in a nonclassical cadherin-mediated functions. They can be used for e.g.

comprising adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug the atumour in a mammal, treating cancer in a mammal, inhibiting or treating apoptosis in a mammal, inhibiting or treating or treating obesity in a mammal, inhibiting cell, preventing or treating obesity in a mammal, inhibiting scar, to the captressing cell, preventing or treating demylinating neurological disease, central nervous system, treating a demylinating neurological disease, central nervous system, treating a demylinating neurological disease, central nervous system, treating cells, inhibiting synaptic stability in nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, creating admension of forcign tissue in a correducing or a frecting neurite outgrowth, facilitating wound healing cer reducing scar tissue, or enhancing adhesion of forcign tissue in a credited macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors.

companies and also be used for detection and diagnosis and in bioreactors.

companies and also be used for detection and diagnosis and in bioreactors.

companies and conference of the present specifically claimed peptides, and payeds.

contral exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
  Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-7; cadherin-7; cadherin-1; cadherin-1; cadherin-1; receptor; II-cadherin; protocadherin; cadherin telated neuronal receptor; II-cadherin; protocadherin; reamoglain; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 48; Page 180; 252pp; English.
                                                                                                                                                                                                                                                                          Location/Qualifiers 1..6
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98US-00187859.
99US-00234395.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-NOV-1998;
20-JAN-1999;
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Gaps .. 0

4; Conservative

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The present invention describes cadherin modulating agents (NA)

CC comprising peptides which comprise a nonclassical cadherin cell adhesion

C recognition (ORA) sequence. The MAs can be used for eage

conclassical cadherin-mediated functions. They can be used for e.g.

conclassical cadherin-mediated functions. They can be used for e.g.

cc inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug to a tumour in a mammal, treating canner in mammal, inhibiting any operation of a cancer in a mammal, inhibiting any operation of a cancer in a mammal, inhibiting any calls, preventing or treating obesity in a mammal, stimulating conversesing cell, preventing or treating obesity in a mammal, stimulating central nervous System, treating a demyelinating neurological disease, central nervous System, treating a demyelinating neurological disease, contral nervous System, in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in neurological disease, nonclassical cadherin-expressing cells, inhibiting synaptic stability in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age mammal. They can also be used for the scar and diabetes. The products can also be used for detection and diabetes and proceducts can also be used for detection and diabetes.
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                                                                                                                                                                                                                                            Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-7; cadherin-15; cadherin-16; T-cadherin; PB-cadherin; protocadherin; cadherin-16; T-cadherin; pB-cadherin; protocadherin; democratical receptor; LI-cadherin; protocadherin; cadherin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                             Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3573.
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AAY64259 standard; peptide; 6 AA.
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99US-00234395.
99US-00264516.
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20-JAN-1999;
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(first entry)

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AAY62757 standard; peptide; 6 AA.
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                                                                                                                         RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic antiinflammatory peptide derived from IL-2 and its derivatives useful for treating inflammatory autoimmune diseases such as rheumatoid arthritis, multiple sclerosis and systemic lupus erythematosus.
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                                                                                                           Gaps
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                                                                                                           1; Indels
                                                           Length 6;
                                                           Score 24; DB 3; I
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL-2 derived anti-inflammatory peptide pep11.
                                                                                                                 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           AAY85373 standard; peptide; 6 AA.
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98IL-00126009.
99IL-00129980.
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                                                                 63.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                    Local Similarity 50.0
nes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-256367/22.
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1 CDPVSC 6
                                                                                                                                                                            1 CVPLTC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-1998;
16-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1999;
                Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAY85373;
                                                                         Query Match
                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                 RESULT 7
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The present invention describes cadherin modulating agents (MA)

CC comprising peptides which comprise a nonclassical cadherin cell adhesion

C recognition (CAR) sequence. The MAs can be used for modulating

recognition (CAR) sequence. The MAs can be used for modulating

conclassical cadherin-mediated functions. They can be used for e.g.

conclassical cadherin-mediated functions. They can be used for e.g.

conclassical adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cc ampressing cell, preventing or treating obesity in a mammal, stimulating capressing in a mammal, enhancing delivery to the correasing vasopermeability in a mammal, enhancing delivery to the increasing vasopermeability in a mammal. They can also be used for conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal. They can also be used for conclassing and diabetes. The related macular degeneration, multiple sclerosis and in bioreactors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                  inhibition; cadherin extracellular domain; cell adhesion recognition; cadherin-5; cadherin-6; cadherin-7; cadherin-13; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin-14; cadherin-16; T-cadherin; PB-cadherin; protocadherin; cadherin; desmoglein, desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                             PB-cadherin cell adhesion recognition cyclic peptide SBQ ID NO:4040.
                                                                                                       Modulation; nonclassical cadherin mediated cell adhesion; CAR;
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 72; Page 193; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gour BJ, Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00073040.
98US-00187859.
99US-00234395.
99US-00264516.
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Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAY-1999;
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20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1998;
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                                                                                                                                                                                                                                                                                                            Synthetic
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Gaps

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60.5%; Score 23; DB 3; Length 6; 50.0%; Pred. No. 1.40+06; Live 1; Mismatches 2; Indels

Best Local Similarity 50.0 Matches 3; Conservative

Query Match

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RESULT 10
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ID AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin—mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a cauge through the skin of a mammal, and inhibiting a mammal, inhibiting an aningly of a cancer in a mammal, inhibiting aningly and aningly and an aningly and an inhibiting expressing cell, preventing or treating obesity in a mammal, stimulating expressing cell, preventing or treating obesity in a mammal, stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; cadherin; cadherin-6; cadherin-6; cadherin-7; cadherin-8; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin calated neuronal receptor; II cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid archritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
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AAY60592 to AAY64572 represent specifically claimed peptides, and AAV64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used the exemplification of the present invention
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cadherin-15 cell adhesion recognition cyclic peptide SEQ ID NO:2154.
                                                                                                                                                                                             .
0
                                                                                                                                         Score 23; DB 3; Length 6; pred. No. 1.4e+06; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 60; Page 188; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                AAY62488 standard; peptide; 6 AA.
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                                                                                                                                                   60.5%;
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                                                                                                                                                                                                    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .6
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                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                   1 CVPLTC 6
                                                                                                                                                                                                                                                                                               CDELTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blaschuk OW,
                                                                                                            Sequence 6 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09957149-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY62488;
                                                                                                                                                          Query Match
                                                                                                                                                                                                         Matches
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AAY62488
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blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of monclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, inhibiting synaptic stability in a mammal, or preventing pregrancy in a mammal. They can also be used for a mammal. They can also be used for treating edhesion of foreign tissue in a correducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The related macular degeneration, multiple sclerosis and diabetes. The ARX60592 to AAX64572 represent specifically claimed peptides, and AX33188 to AAX64573 to AAX64531 to AAX33188 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is a peptide fragment derived from domain 1 of human beta-2 glycoprotein, a phospholipid binding serum protein. Isolated domain 1 of beta-2 GPI protein binds to and inhibits beta-2 GPI-dependent antiphospholipid antibodies. The fragments are useful as toleragens when they bind to the antibodies at the surface of a B cell and triggers B cell anergy. The polypeptides and mimetics can be used for treating disorders associated with beta 20PI-dependent aPL-associated pathologies, e.g. thrombosis, recurrent foetal loss, thrombosytopenia or autoimmune diseases such as systemic lupus erythematosus. The polypeptides can also be used to detect and purify antibodies. They can also be used in
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human beta-2 glycoprotein I; beta-2 GPI; toleragen; B cell anergy; beta-2 GPI-dependent antiphospholipid antibody; thrombosis; recurrent foetal loss; thrombocytopenia; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide 1 derived from domain 1 of human beta-2 glycoprotein I.
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                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                     Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               systemic lupus erythematosus; coagulation assay.
                                                                                                                                                                                                                                                                                                                                                   Score 23; DB 3; L
Pred. No. 1.4e+06;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 19; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44431 standard; peptide; 6 AA.
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99US-00328199.
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                                                                                                                                                                                                                                                                                                                                                       66.7%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDELTC 6
                                                                                                                                                                                                                                                                                                                   Sequence 6 AA;
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08-JUN-1999;
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Query Match

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Best Loc Matches

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Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include a family of tetrapeptides based on the recognition site (AAR49776) of farnesyltransferase (FT), are potential anticancer agents that inhibit FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                         New farnesyl-transferase inhibitors - used for inhibiting attachment of a farnesyl moiety to a p21ras protein in malignant cells.
                                                                                                                                Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras; ras protein; farnesylation; cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Farnesyl transferase; inhibitor; cancer; ras; p21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%; Score 22; DB 2; I
75.0%; Pred. No. 1.4e+06;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   Goldstein JL, Reiss Y, Marsters JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 33; 183pp; English.
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AAR49769 standard; peptide; 4 AA.
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                                                                                                        Farnesyltransferase-inhibitor.
                                                                                                                                                                                                                                                                              93WO-US008062.
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(first entry)
                                                             (revised)
(first entry)
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Best Local Similarity
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23-JAN-1996
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                                                                                                                                                                                                                                                                                                          24-AUG-1992;
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                                                                                                                                                                                                                  WO9404561-A1
                                                              25-MAR-2003
                                                                             08-AUG-1994
                                                                                                                                                                                                                                                 03-MAR-1994.
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                                                                                                                                                                                                                                                                                                                                                                                        Brown MS,
                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR77833;
                                 AAR49769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This peptide or the peptides represented in AAR15751-81, AAR14723 and AAR14711 inhibit the rat FTS represented in AAR14712-22. They show FT inhibition at an ICSO of 0.01-10 micros. The most potent inhibitors are ones in which phenylalanine occurs at the third position of a crespic whose N-terminus is cysteine. The inhibitors have a farnesylacceptor or inhibitor sequence within its structure and are capable of inhibiting the farnesylation of p21ras by FT. See also AAR14711-23 and AAQ14541-47. (Updated on 09-UAN-2003 to add missing OS field.) (Updated on 02-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compsn. comprising purified farnesyl-protein transferase - used to inhibit attachment of farnesyl moiety to RAS protein in malignant cells
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                                                                                                  Gaps
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                                                                 60.5%; Score 23; DB 3; Length 6; 50.0%; Pred. No. 1.4e+06; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Farnesyl; transferase; FT; inhibitor; p21ras; rat.
                                                                                                                                                                                                                                                                                                                                                            Farnesyl-protein transferase inhibitor (25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goldstein JL, Reiss Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; Page 68; 87pp; English.
                                                                                                                                                                                                                                         AAR15772 standard; protein; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-00510706.
90US-00615715.
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                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TEXA ) UNIV TEXAS SYSTEM
                                                                                                     3; Conservative
                                                                                                                                                                                                                                                                                                    (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-339750/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                   Local Similarity
         coagulation assays
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1 CVPM 4
                                                                                                                                1 CVPLTC 6
                                                                                                                                                               CTPRVC 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4 AA;
                                         Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-APR-1990;
                                                                                                                                                                                                                                                                                                    25-MAR-2003
09-JAN-2003
29-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9116340-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-OCT-1991
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Brown MS,

RESULT 12 AAR49769

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Synthetic.

AAR15772;

RESULT 11 AAR15772

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Gaps ; 0

0; Indels Length 4;

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1 CVPL 4
                                                                                                                                                     CVPM 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Disulfide-bond
                                                       K-RasB protein
                                                                                                                                                                                                                                                                                                                                                      Modified-Bite
                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                        Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    JP10226698-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-AUG-1998.
                                                                                                                                                                                                                                            02-MAR-1999
                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                        AAW67428;
                                                                                                                                                                                    RESULT 15
                                                                                                                Matches
                                                                                                                                                                                              AAW67428
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                                                                                                                                          ARK77800, AAR77805-R77838 are tetrapeptide inhibitors of farnesyl transferase. They all obey a generic formula for the C-terminal sequence of 4-10 amino acid inhibitory peptides; the formula is -CAAX, where C=cysteine, A= any aliphatic, arcmatic or hydroxy amino acid and X= any normal amino acid. Farnesyl transferase is involved in the farnesylation of various cellular proteins including the cancer related ras proteins. The transforming activity of ras is dependent on the localisation of the protein to membranes, a property which is thought to be dependent upon the addition of farnesyl groups. The peptide inhibitors are useful for the activity and ras-related cancers in particular. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                     New farnesyl transferase inhibitor peptide(s) - based on farnesyl acceptor substrate carboxy terminal sequences, used for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assay for farnesyl transferase activity - by determining ability to transfer farnesyl molety to K-Ras B protein, partic. useful for identifying inhibitors.
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl; ras protein; K-ras B; malignant; detection; identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Farnesyl transferase peptide inhibitor used in cancer treatment.
                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                      Length 4;
                                                                                                                                                                                                                                                                                     Score 22; DB 2; I
Pred. No. 1.4e+06;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 34; 257pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GĽ,
                                                                                                                                                                                                                                                                                                                                                                                                  AAW04459 standard; peptide; 4 AA.
                                                  Brown MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  James
                                                                                                                                Claim 2; Col 62; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96MO-US005969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00429964
                                                                                                                                                                                                                                                                                         57.9%;
75.0%;
   90US-00615715.
92US-00822011.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goldstein JL,
                                                                                                                                                                                                                                                                                                Local Similarity 75.0
                                                   Goldstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-497642/49.
                                                                       WPI; 1995-206308/27.
                               (TEXA ) UNIV TEXAS.
                                                                                                                                                                                                                                                                                                                                             1 CVPL 4
                                                                                                                                                                                                                                                                       Sequence 4 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TEXA ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9634113-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-0CT-1996
     20-NOV-1990;
16-JAN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW04459;
                                                                                                                                                                                                                                                                                         Query Match
                                                     Reiss Y,
                                                                                                                cancer.
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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This sequence represents an analogue peptide of the Hepatitis C virus (HCV) nucleocapsid core protein. The invention relates to peptide analogues derived from HCV proteins, e.g. ANWGATI-WGYAG, which can be used for the determination of anti-HCV antibodies in a sample. Preferably the peptide analogues contain one or more thioamide peptide bonds where at least one oxygen atom of the peptide bond is replaced by sulphur atom. The peptide analogues can be adsorbed or chemically bound to a carrier
                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                               to
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleocapsid; core protein; analogue; antibody; thioamide bond; peptide bond.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of antibody in sample - uses peptide analog absorbed or chemically bound on carrier as antigen.
AAW04433-W04465 are peptide inhibitors of farnesyl transferase (FT) activity. The peptides block the attachment of prenyl groups to ras proteins in malignant cells of patients suffering from cancer or a precancerous state and as such are used to treat cancer. The peptides were identified by determining the ability of candidate substances to inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety to
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and C-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "side chain protected by benzoyl group
terminus protected by benzyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "side chain protected by tosyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "side chain protected by butyl group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5;
                                                                                                                                                                                                                                                                                        Length 4;
                                                                                                                                                                                                                                                                                                            Pred. No. 1.4e+06;
1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 2; 1 Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                        Score 22; DB 2;
Pred. No. 1.4e+06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 9; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW67428 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.9%;
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                                                                                                                                                                                                                                                                                              57.9%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                        3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV peptide analogue #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; HCV;
non-structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KYOW ) KYOWA MEDEX KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-515103/44
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Best Local Similarity
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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 Matches
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 Conservative
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 Mismatches
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 Gaps

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Search completed: March 8, 2004, 12:37:06 Job time : 53 secs

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March 8, 2004, 12:38:25; Search time 33 Seconds (without alignments) 38.392 Million cell updates/sec
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| cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*
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| cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*
| cgn2_6/prodata/2/pubpaa/USO0_NEW_PUB.pep:*
| cgn2_6/prodata/2/pubpaa/USOO_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                809742 seqs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-761-636A-12
38
1 CVPLTC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 12, Appl	Sequence 1374, Ap	Sequence 1374, Ap	Sequence 1798, Ap	Sequence 3970, Ap	Sequence 4046, Ap	Sequence 1798, Ap	Sequence 3970, Ap	_		Sequence 3573, Ap	Sequence 2154, Ap		Sequence 2154, Ap	Sequence 4040, Ap
SUMMARIES		ID	US-09-761-636A-12	. US-10-006-869-1374	US-10-395-032-1374	. US-10-006-869-1798	US-10-006-869-3970	US-10-006-869-4046	S US-10-395-032-1798	S US-10-395-032-3970	5 US-10-395-032-4046	US-10-006-869-3573	S US-10-395-032-3573	1 US-10-006-869-2154	1 US-10-006-869-4040	S US-10-395-032-2154	5 US-10-395-032-4040
		Query Match Length DB	6 9	6 14	6 15	6 14	6 14	6 14	6 15	6 15	6 15	6 14	6 15	6 14	6 14	6 15	6 15
	₩	Query Match I	100.0	68.4	68.4	65.8	65.8	65.8	65.8	65.8	65.8	63.2	63.2	60.5	60.5	60.5	60.5
		Score	38	26	26	25	25	25	25	25	25	24	24	23	23	23	23
		Result No.		2	m	4	ហ	9	7	80	6	10	11	12	13	14	15

	Sequence 103, App	1737,	Sequence 2719, Ap			184,	Sequence 186, App	222	526	278		~		Seguence 1885, Ap	277	ω.	90	92	94,	9		52,			7	5		Sequence 210, App	
US-10-083-894-35	US-09-943-944E-103	US-10-006-869-1737	US-10-006-869-2719	US-10-395-032-1737	US-10-395-032-2719	US-09-911-838-184	US-09-911-838-186	US-09-792-286-222	US-09-792-286-226	ns-		US-10-006	US-10-058-513-9		US-10-	US-09-753-139C-8	US-09-911-838-	US-09-911-838-92	US-09-911	US-09-911-838-96	US-10	US-10		US-10		US-10-395-032-1591	US-09-234-395-124	US-09-234-395-210	US-09-305-928-124
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ALIGNMENTS

US-09-761-636A-12

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Gaps
Sequence 12, Application US/09761636A;
Sequence 12, Application US/09761636A;
Patent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHARN, Marc
APPLICANT: ACRORN, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION WHERE: US/09/761,636A
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT APPLICATION NUMBER: US/0176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.0%; Score 38; DB 9; Length 6; Similarity 100.0%; Pred. No. 7.2e+05; 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Homo sapiens
US-09-761-636A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVPLTC 6
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; Sequence 1374, Application US/10006869 ; Publication No. US20030082166A1

RESULT 2 US-10-006-869-1374

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Gaps

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Sequence 4046, Application US/10006869
; Sequence 4046, Application US/10006869
; Publication No. US2030082166A1
; Publication No. US2030082166A1
; GENERAL INFORMATION:
    APPLICANT: Symonds, James Matthew
    APPLICANT: Symonds, James Matthew
    APPLICANT: Symonds, James Matthew
    TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
    TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
    TITLE OF LING DATE: 2001-12-03
    CURRENT APPLICATION NUMBER: 12/10/006,869
    CURRENT FILING DATE: 2001-12-03
    SOFTWARE: PatentIn Ver. 2.0
    SEQ ID NO 4046
    LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3970, Application US/10006869;
Sequence 3970, Application US/10006869;
Publication No. US20030082166A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.4077;
CURRENT PAPLICATION NUMBER: US/10/006,869
CURRENT PAPLICATION NUMBER: US/10.12-03
CURRENT PAPLICATION NUMBER: 2001-12-03
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: Representative cyclic modulating agent based on
CTHER INFORMATION: cadherin-14 cell adhesion recognition sequence
US-10-006-869-3970
                                                                                                                                                                                                                                               OTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-12 cell adhesion recognition sequence US-10-006-869-1798
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                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 14; Length 6; Pred. No. 7.2e+05; 0; Mismatches 2; Indels
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO 1798
LENGTH: 6
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Best Local Similarity 66.7%;
Matches 4; Conservative
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Best Local Similarity
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APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
IITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CACHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.40777
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APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C9
CURRENT APPLICATION NUMBER: US/10/395,032
CURRENT APPLICATION NUMBER: US/10/395,032
SUFRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
                                                                                     APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT PILING DATE: 2001-12-03
NUMBER: OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1374
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Publication No. US20030082166A1
GENERAL INFORMATION:
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                                                              APPLICANT: Blaschuk, Orest W. APPLICANT: Symonds, James Matthew
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US-10-006-869-1798
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; bublication No. US20030082166A1
; GENERAL INFORMATION:
    APPLICANT: Blaschuk, Orset W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Symonds, James Matthew
; APPLICANT: Cour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHENIAN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.4077
; CURRENT APPLICATION NUMBER: US/10/006,869
; UNMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3573
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APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHER: US/10/395,032
CURRENT APPLICATION NUMBER: US/10/395,032
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO 4446
LENGTH: 6
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                                   Indels
Similarity 66.7%; Pred. No. 7.2e+05; 4; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                    Sequence 4046, Application US/10395032; Publication No. US20030229199A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 50.03
Matches 3; Conservative
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              Best Local Similarity
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US-10-006-869-3573
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US-10-395-032-4046
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| Publication No. US20030229199A1
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. | APPLICANT: Blaschuk, Orest W. | APPLICANT: Symonds, James Matthew APPLICANT: Symonds, James Matthew APPLICANT: Cour. Barbara J. | TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL | TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS | TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS | FILE REPRENCE: 100006.40705 | CURRENT APPLICATION NUMBER: US/10/395,032 | CURRENT FILING DATE: 2003-03-21 | NUMBER OF SEQ ID NOS: 4052 | SOFTWARE: Patentin Ver. 2.0 | SEQ ID NOS: 4052 | SEQ
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                                                            FEATURE: OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence
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Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 0; Mismatches 2; Indels
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; Sequence 1798; Application US/10395032; Publication No. US20030229199A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-10-395-032-3970
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US-10-006-869-4046
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65.8%; Score 25; DB 15; Length 6;

Query Match

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TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.74
These 4; Conservative
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GENERAL INFORMATION:
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US-10-395-032-2154
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Publication No. US20030082166A1
GENERAL INFORMATION:
APPLICAMT: Blaschuk, Orest W.
APPLICAMT: Symonds, James Matthew
APPLICAMT: Symonds, James Matthew
APPLICAMT: Symonds, James Matthew
APPLICAMT: Gour, Barbara J.
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
CURRENT PILIAM DATE: 2001-12-03
CURRENT FILIAM DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2154
                                                                            Sequence 3573, Application US/10395032

Publication No. US20030229199A1

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: CADHERIN MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN MEDIATED FUNCTIONS
FILE REFERENCE: 100086.4070;
CURRENT APPLICATION NUMBER: US/10/395,032
CURRENT PILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NOS: 3573
LEWARD: ALLOHOUSED FUNCTIONS
SEQ ID NOS: 4052
SEQ ID NOS: 4052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.2%; Score 24; DB 15; Length 6; 50.0%; Pred. No. 7.2e+05; tive 2; Mismatches 1; Indels
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; Sequence 4040, Application US/10006869
; Publication No. US20030082166A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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Matches 3; Conserv
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                                                        RESULT 11
US-10-395-032-3573
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Sequence 2154, Application US/10395032
| Sequence 2154, Application No. US20030229199A1
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W. |
| APPLICANT: Symonda James Matthew |
| APPLICANT: Symonda James Matthew |
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL |
| TITLE OF INVENTION: COMPOUNDS |
| TITLE OF INVENTION: COMPOUNDS |
| TITLE OF INVENTION: CADABRENIA-MEDIATED FUNCTIONS |
| FILE REFERENCE: 100086.407C9 |
| CURRENT APLICATION NUMBER: US/10/395,032 |
| CURRENT APLICATION NUMBER: US/203 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NOS: 4052 |
| SEQ ID NOS:
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Sequence 4040, Application US/10395032

Publication NO. US20330229199A1

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CAPHERIN-MEDIATED FUNCTIONS

FILE REFERENCE: 100086.407C9
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
CURRENT APPLICATION NUMBER: US/10/06,869
CURRENT APPLICATION NUMBER: US/10/06,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO 4440
LENGTH: 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: PB-cadherin cell adhesion recognition sequence US-10-006-869-4040
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CURRENT APPLICATION NUMBER: US/10/395,032

CURRENT FILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 4052

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4040

LENGTH: 6

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FRATURE:

OTHER INFORMATION: Representative cyclic modulating agent based on order information of the in
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rucelalti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Pasqualini, Renata
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
TITLE OF INVENTION: Membrane Dipeptidase
TITLE OF INVENTION: Membrane 198/09/258,754
CURRENT APPLICATION NUMBER: 09/042,107
ERALIER PILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARE: ParentIn Ver. 2.0
SEQ ID NO 199
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; Patent No. 6174687
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ORGANISM: Artificial Sequence
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US-09-258-754-199
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SEQ ID NO 34
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TYPE: PRT
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Sequence 199, App
Sequence 199, App
Sequence 3614, Ap
Sequence 199, App
Sequence 25, Appl
Sequence 25, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 30, Appl
Sequence 10, Sepl
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Sequence 43, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 17, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 38, Appl
Sequence 48, Appl
Sequence 48, Appl
Sequence 49, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 67, Appl
Sequence 67, Appl
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                                                                                                March 8, 2004, 12:16:07; Search time 15.5 Seconds (without alignments) 29.976 Million cell updates/sec
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3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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3. /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
3. /cgn2_6/ptodata/2/iaa/pacKfilesI.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-256-754-199
US-09-042-107-199
US-09-187-859-3614
US-09-183-542B-3614
US-09-183-542B-3614
US-09-183-542B-3614
US-09-760-599-25
US-08-483-550B-25
US-08-483-434A-21
US-08-476-134A-30
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5506208-28
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US-08-462-018-43
US-08-602-483-49
US-09-760-599-17
US-09-760-599-17
US-09-760-599-18
US-09-481-550B-9
US-09-481-550B-9
US-09-481-550B-9
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US-08-481-550B-9
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Maximum Match 100%
Listing first 45 summaries
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Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 14, Appli
Sequence 146, Appl
Sequence 122, Appl
Sequence 122, Appl
Sequence 122, Appl
Sequence 122, Appl
Sequence 138, Appl
Sequence 138, Appl
Sequence 23, Appl
Sequence 25, Appl
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                                                                                                           US-08-414-4178-3
US-08-66-5458-3
US-08-66-5458-3
US-08-66-5458-3
US-08-66-6808-3
US-09-258-754-146
US-09-258-754-308
US-09-139-802-92
US-09-042-107-308
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US-09-16-513-122
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Larson Mr., Richard S.
APPLICANT: Larson Mr., Richard S.
APPLICANT: Larson Mr. Peptide Inhibitors of LFA-1/CAM-1 Interaction FILE REFERENCE: SCI200/4-1CIP
FILE REFERENCE: SCI200/4-1CIP
CURRENT APPLICATION NUMBER: US/09/760,599
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
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33.3%; Pred. No. 3e+05;
tive 4; Mismatches
; Sequence 34, Application US/09760599
; Patent No. 6630447
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Best Local Similarity
Matches 3; Conserv
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Sequence 199, Application US/09722250D
; Sequence 199, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Ragqualini, Renata
; TITLE OF INVENTION: Tissues
; TITLE OF INVENTION: DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; WRICH FILING DATE: 1998-03-13
                                                                                                Sequence 3614, Application US/09839542B

Sequence 3614, Application US/09839542B

Patent No. 665996

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
ITILE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
ITILE REFRERENCE: 100064.407D1
CURRENT APPLICATION NUMBER: 105/09/839,542B
CURRENT PELLING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
ILROTATE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion OTHER INFORMATION: recognition sequence
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Pred. No. 3e+05;
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55.6%; Pred. No. 3e+05;
tive 0; Mismatches '
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Best Local Similarity 44.4%;
Matches 4; Conservative 2
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 199
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Matches 5; Conserv
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1 CTFHIDSVC 9
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US-09-722-250D-199
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Patent No. 6358920

GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Corest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE REFERENCE: 100086, 40701.
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052

SEQ ID NOS: 4052

SEQ ID NOS: 4052

SEQ ID NO 3614
                                                                                                                                                                                                                                                                                                                                       Sequence 199, Application US/09042107;
Sequence 199, Application US/09042107;
Patent No. 623289;
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Tissues
TITLE REFERENCE: P-LJ 2892
CURRENT FILING DATE: 1998-03-13
CURRENT FILING DATE: 1998-03-13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO. 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-199
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                          ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-199
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                                                                                                                                                     4; Indels
                                                                                                            Length 9;
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Pred. No. 3e+05;
                                                                                                         50.0%; Score 25; DB 3; 55.6%; Pred. No. 3e+05; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                     Query Match 50.0
Best Local Similarity 55.6
Matches 5; Conservative
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US-09-187-859-3614
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US-09-187-859-3614
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US-09-042-107-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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Gaps

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Gaps

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RESULT 7 US-09-760-599-25

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Gaps

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3; Indels

50.0%; Score 25; DB 4; Length 9; 44.4%; Pred. No. 3e+05;

2; Mismatches

4; Conservative

Query Match Best Local Similarity Matches 4; Conserv

1 CSVPLTSVC 9

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Query Match
Best Local Similarity
Matches 4; Conserv
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US-08-476-134A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Larson Mr., Richard S.
APPLICANT: Larson Mr., Richard S.
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
TITLE OF INVENTION: PSC1200/4-001
CURRENT APPLICATION NUMBER: US/09/483,550B
CURRENT FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
                                                 APPLICANT: Larson Mr., Richard S.
APPLICANT: Larson Mr., Richard S.
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
FILE REFERENCE: SCI200/4-ICIP
CURRENT APPLICATION NUMBER: US/09/760,599
CURRENT FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/08483434A
Parent No. 5648401
Patent No. 5648401
Patent No. 5648401
Parent No. 5648401
Parent No. 5648401
Parent No. 5648401
Papilcant: EVAL, Jacob
APPLICANT: HAMILTON, Bruce K.
APPLICANT: TUSZYNSKI, George P.
TITLE OF INVENTION: Synthetic Analogs of Thrombospondin and
TITLE OF INVENTION: Therapeutic Use Thereof
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                   ; CTHER INFORMATION: Description of Artificial Sequence:Synthetic US-09-760-599-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB 4; Length 9; Pred. No. 3e+05;
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ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 Market Street, 36th Floor
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 50.0%; Score 25; DB 4; Best Local Similarity 33.3%; Pred. No. 3e+05; Matches 3; Conservative 3; Mismatches ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/09483550B Patent No. 6649592
Sequence 25, Application US/09760599
Patent No. 6630447
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 50.0%;
Best Local Similarity 33.3%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : |:|
1 CMLRMNSIC 9
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1 CMLRMNSIC 9
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US-09-483-550B-25
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                                                                                                                                                                                                                                                                               TYPE: PRT
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SYAL, JACOB
APPLICANT: HAMILTON, BRUCE K.
APPLICANT: HAMILTON, BRUCE K.
APPLICANT: TUSZYNSKI, GENGER P.
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: 1995-06-07
CURRENT PILLING DATE: 1996-09-24
RRIOR FILING DATE: 1990-09-24
RRIOR PLILING DATE: 1990-09-22
PRIOR PLILING DATE: 1995-06-22
PRIOR FILING DATE: 1995-06-22
PRIOR PLILING DATE: 1995-06-22
PRIOR PLILING DATE: 1995-06-22
PRIOR PLILING DATE: 1995-06-25
PRIOR PLILING DATE: 1995-06-25
PRIOR PLILING DATE: 1995-06-25
PRIOR PLILING DATE: 1996-01-24
PRIOR PLILING DATE: 1994-01-24
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COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compactible
COMPUTER: IBM PC compactible
COMPUTER: IBM PC compactible
COMPUTER: IBM PC compactible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,434A
FILING DATE: 07-JUN-1995
FILING DATE: 25-MAY-1995
PRIOR APPLICATION NUMBER: US 08/185,614
PRIOR APPLICATION NUMBER: US 08/185,614
PRIOR APPLICATION NUMBER: US 08/24,436
FILING DATE: 24-JAN-1994
PRIOR APPLICATION NUMBER: US 07/587,197
FILING DATE: 24-SEP-1990
PRIOR APPLICATION NUMBER: US 07/483,527
FILING DATE: 22-FEB-1990
PRIOR APPLICATION NUMBER: US 07/483,527
FILING DATE: 22-FEB-1990
PRIOR APPLICATION NUMBER: US 07/483,527
FILING DATE: 22-FEB-1990
ATTORNEY/AGRAT INFORMATION:
NAME: Leasy Ph.D., Kathryn
REGISTRATION NUMBER: 35,317
REGISTRATION NUMBER: 35,317
REGISTRATION NUMBER: 35,317
REGISTRATION NUMBER: 35,217
TELECHONE: CLASA TUBER: 35,317
TELECHONE: Leasy Ph.D., Kathryn
REGISTRATION NUMBER: 35,217
TELECHONE: CLASA TUBER: 35,317
TELECHONE: CLASA TUBER: 35,317
TELECHONE: CLASA TUBER: 35,317
TELECHONE: GARNATION: ACCORDING TELECHONE: (215) 567-2991
TELECHONE: GARNATION SCORE IN SEQUENCE: SEQUENCE: AMPLOR ACCORDING TELECHONE: CLED.
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches <sup>C</sup>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                APPLICANT: Levis, Michael B.
APPLICANT: Levis, Michael B.
APPLICANT: Sauer, James C.
APPLICANT: Sauer, James C.
APPLICANT: Salison, Kathleen V.
APPLICANT: Callison, Kathleen V.
APPLICANT: Baldino, Frank
APPLICANT: Igbal, Mohamed
TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
TITLE OF INVENTION: ADALOGS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STERET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 44.4%; Pred. No. 36+05;
Matches 4; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTER TEADABLE FORM:

ZIP: 02110-2804

COMPUTER READABLE FORM:

REDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: BM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOSTWARE: WordPerfect (version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/958,903A

FILING DATE: October 7, 1992

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/534,139

FILING DATE: June 5, 1990

APPLICATION NUMBER: 07/669,913

FILING DATE: June 5, 1990

APPLICATION NUMBER: 07/669,913

FILING DATE: APPLI 15, 1992

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 02655/003004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-08-462-018-43
Sequence 43, Application US/08462018
Parent No. 5703045
GENERAL INFORMATION:
APPLICANT: Lewis, Michael E.
                                                                               Sequence 43, Application US/07958903A. Patent No. 5652214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTPAKSEC 9
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boston
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US-07-958-903A-43
                                                                          JS-07-958-903A-43
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                                                     RESULT 13
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                                                                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: analog of thrombospondin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEORGE P.
TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS OF TITLE OF INVENTION AND AND AND AND APPLICATION NUMBER: US/08/408,181
APPLICATION NUMBER: US/08/408,181
FILING DATE: 22-MAR-1995
FRICK APPLICATION NUMBER: 131,565
FRICK APPLICATION NUMBER: 985,764
FILING DATE: 09-UW-1992
FILING DATE: 09-UW-1992
FILING DATE: 24-SEP-1990
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.0%; Score 24; DB 6; Length 6; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                              Ouery Match 48.0%; Score 24; DB 3; Length 6; Best Local Similarity 100.0%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHOD FOR USING SYNTHETIC ANALOGS
OF THROMEOSPONDIN FOR INHIBITING METASTASIS ACTIVITY
NUMBER OF SEQUENCES: 32
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/587,197
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: EYAL, JACOB, HAMILTON, BRUCE K., TUSZYNSKI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
519080-26
Patent No. 5190920
A APPLICANT: EYAL, JACOB,HAMILTON, BRUCE K.,TUSZYNASKI,
PRIOR FILING DATE: 1993-03-01
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.03
Matches 4; Conservative
                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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;Patent No. 5506208
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                                                                                                                                                                                                                                  US-08-476-134A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:28:
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Ouery Match 48.0%; Score 24; DB 1; Length 9; Best Local Similarity 44.4%; Pred. No. 3e+05; Matches 4; Conservative 0; Mismatches 5; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CUMPULER: 552A
CUMPULER: 552A
COMPULER: 552A
SOFTWARE: WordPerfect (Version 5.0)
SOFTWARE: 4.19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823,245
FILING DATE: March 24, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/361,595
FILING DATE: June 6, 1980
APPLICATION NUMBER: 07/534,139
FILING DATE: June 6, 1990
APPLICATION NUMBER: 07/586,903
FILING DATE: APPLI 15, 1992
APPLICATION NUMBER: 07/958,903
FILING DATE: OCLOBER 7, 1992
APPLICATION NUMBER: 07/958,903
FELENENCE/DOCKET NUMBER: 02655/003008
TELEFAX: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                  APPLICATION
OF INSULIN-LIKE GROWTH
FACTORS AND
ANALOGS
                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or
COMPUTER: 55SX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 8, 2004, 12:21:08 Job time : 15.5 Becs
                                                               TITLE OF INVENTION: APPLICATION.
TITLE OF INVENTION: OF INSTLIN-L.
TITLE OF INVENTION: FACTORS AND
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSERS: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
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STRANDEDNESS: N/A
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APPLICANT: Kauer, James C.
APPLICANT: Smith, Kevin R.
APPLICANT: Callison, Kathleen V.
APPLICANT: Callison, Kathleen V.
APPLICANT: Nofela
APPLICANT: Hoff, Nicola
APPLICANT: Hoff, Nicola
TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STRYE: Massachusetts
COUNTRY: U.S.A.
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 18M PS/2 Model 50Z or 55SX
COMPUTER: 18M PS/2 Model 50Z or 55SX
COMPUTER: 18M PS/2 Model 50Z or 55SX
COMPUTER: 18M PS/2 Model 5.0
SOBTWARE: Worderfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/08/462,018
FILING DATE: COTOBER: 7,1992
APPLICATION NUMBER: 07/958,933
FILING DATE: OCTOBER 7,1992
APPLICATION NUMBER: 07/361,595
FILING DATE: June 5,1990
APPLICATION NUMBER: 07/869,913
FILING DATE: June 5,1990
APPLICATION NUMBER: 07/869,913
FILING DATE: APPLI 15,1992
APPLICATION NUMBER: 07/869,913
FILING DATE: APPLI 15,1990
APPLICATION NUMBER: 07/869,913
FILING DATE: APPLICATION NUMBER: 07/869,913
APPLICATION NUMBER: 07/869,913
APPLICATION NUMBER: 07/869,913
APPLICATION NUMBER: 0
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APPLICANT: Iqbal, Mohamed
TITLE OF INVENTION: TREATING DISORDERS BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 43, Application US/08823245; Patent No. 5776897
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APPLICANT: Lewie, Michael
APPLICANT: Kauer, James C.
APPLICANT: Smith, Kevin R.
APPLICANT: Callison, Kathleen V.
APPLICANT: Baldino, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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Gaps 0;

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March 8, 2004, 12:27:23 ; Search time 20 Seconds (without alignments) 33.667 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                        283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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42
1 CVPLTSC 7
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                                Searched:
                                                                                                      Run on:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	R-phycoerythrin al glycoprotein compo	MHC HZ-L antigen - vicilin 57K chain	acetylcholinestera	ž	aggrecan - bovine R-phycoerythrin be	MHC H2-K-k cell su	hypothetical prote	~~!	schwannomin - mous	pos	laminin Bl - weste	seed protein ws-5	dinyarologace red	DNA topolsomerase	R-phycoerythrin ga	₽ .	catch-relaxing per	tryptophyllin, bas	maplul II chain	LIDATORE-DIRPHIA	myomodulin - Calli	Ig kappa chain V-1	gal	virotoxin - destro	R-phycoerythrin al	metallothionein-A	
£	B22565 H48394	I65546	A34026	E60274	S42620	167345	S08606	A32039	154357	A60521	149421	E61491	I48105	148086	F22565	137263	ECMUCR	A61081	838516	PT0087	A28340	E30608	I56695	A58725	A22565	I51049	
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RESULT 3

11.4 4 2 \$43959	RESULT 1 B22565 R.phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment) C.Species: Gastroclonium coulteri C.Species: Gastroclonium coulteri C.Species: Gastroclonium coulteri C.Species: O7-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993 C.Accession: B22565 R.Klotz, A.V.; Glazer, A.W.; Glazer, A.W.; Glazer, A.W.; Glazer, A.W.; Glazer, A.W.; Glazer, A.W.; Mille: Chem. 260, 4856-4863, 1985 A.Fitle: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A22555; MUID:85182601; PMID:3886644 A;Accession: B22565 A,Molecule type: protein A;Residues: 1-5 < KLO>	similarity 100.0%; Pred. No. 2.8e+05; Similarity 100.0%; Pred. No. 2.8e+05; Si Conservative 0; Mismatches 0; Indels 0; Gaps 0; CVP 3 2 CVP 4	RESULT 2 H48394 Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (Cjgecises: Bos Prindigenius taurus (cattle) Cjbate: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997 CjAccession: H48394 R;Mather, I.H.; Banghart, L.R.; Lane, W.S. Bjochem. Mol. Biol. Int. 29, 545-554, 1993 A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-F II-like sequences. A;Reference number: A48394; MUID:93250576; PMID:8485470 A;Archesion: H48394	<pre>preliminary le type: protein set le cApte: protein mental source: milk sequence extracted from NCBI backbone (NCBIP:131518) da: glycoprotein Match Match</pre>	PLTSC 7 ELLGC 6
	rin alph nr-1988 nr-1988 ng-2565 nr 260, racteriz number: pg-555 pg-5565	imilar ; con CVP 3	ompone prim: -1993 48394 ; Bang Biol. ces. mber:	limina limina -6 cMpr -6 cMpr l sour noce ex lycopr lycopr Csimila 3; Co	VEL -
0 1 0 W 4 N N L 8 0 0 1 1 U W 4 N N N N N N N N N N N N N N N N N N	RESULT 1 B22565 R-phycoerythrin alpha-2 ch C;Species: Gastroclonium c C;Accession: B22565 R;Klotz, A.V.; Glazer, A.N. R;Klotz, A.V.; Glazer, A.N. A;Title: Characterization A;Reference number: A25565 A;Accession: B25565 A;Molecule type: protein A;Residues: 1-5 <klo></klo>	Query Match Best Local Si Matches 3;	LT 2 oprotein co oprotein co cossion: Here, 19-Nov cossion: Here, 11-Nov cossion: Here, 11-Nov cossion: Here m	A,Status: preil: A,Status: preil: A,Residues: 1-(A,Residues: 1-(A,	1
8 6 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	RESULT B22565 R-phyc C;Spec C;Acce C;Acce C;Acce A;Riot A;Riot A;Refe A;Refe	Marie Marie Do	RESULT H48394 G1900 G1900 C1900 C2000 C3000 C300	TONE A COME	o d

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major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)

S.Species: Mycobacterium tuberculosis
C.Species: Wycobacterium tuberculosis
C.Species: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C.Spacesion: E60274
S.Nagai, S.N Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect: Immun. 59, 372-382, 1991
A.Fille: Isolation and partial characterization of major protein antigens in the cultural characterization and partial characterization of major protein antigens in the cultural charac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R-phycocrythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment) R-phycocrythrin beta-1 chain - red alga (Gastroclonium coulteri) (Species Gastroclonium coulteri) (Cipate: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993 C; Accession: C22565 Ridor, A.V. Glazer, A.W. Diol. Chem. 260, 4866-4863, 1985 A;Title: Characterization of the bilin attachment sites in R-phycocrythrin. A;Reference number: A22565; MUID:85182601; PMID:3886644 A;Molecule type: protein A;Residues: 1-6 < KLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Bos primigenius taurus (cattle)
C.Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%; Score 14; DB 2; Length 5; 66.7%; Pred. No. 2.8e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S42520
R;Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A;Title: Aggrecan in bovine tendon.
A;Reference number: S42620; MUID:94340214; PMID:7520336
A;Accession: S42620
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A;Residues: 1-7 <VOG>
A;Experimental source: flexor tendon
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Matches 2; Conservative
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Best Local Similarity
Matches 1; Conserv
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A, Molecule type: protein
A, Residues: 1-5 < NAG>
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Best Local Similarity
Matches 2; Conserv
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                               MHC H2-L antigen - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I65546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
Cell 44, 261-272, 1996
A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and theil A;Reference number: I52778; MuID:86106202; PMID:3510743
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C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: B34818
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A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234
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Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A,Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A,Reference number: A34818; MUID:90165956; PMID:2306256
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A;Residues: 1-7 <GIB>
C;Keywords: alternative splicing; carboxylic ester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.7%; Score 15; DB 2; Length 6; ilarity 75.0%; Pred. No. 2.8e+05; Conservative 0; Mismatches 1; Indels
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A, Status: preliminary
A, Molecule type: protein
A, Residues: 1-7 < MAW>
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Gaps

RESULT 9

167345

RESULT 6

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laminin B1 - western wild mouse (fragment)

laminin B1 - western wild mouse (fragment)

(Species 2 Mus spretus (western wild mouse)

C;Decession: 149421

C;Accession: 149421

K;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, C;Accession: 149421

A;Ric, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, C;Accession: 149421

A;Accession: 149421

A;Gratus: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
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Nilternate names a glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Reference number: A60521; MUID:90227907; PMID:2109669
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A,Residues: 1-5 <BON>
C,Superfamily: glucan phosphorylase
C,Superfamily: glycosyltransferase; hexosyltransferase; phosphoprotein
C,Keywords: glycosyltransferase; hexosyltransferase; phosphorylase b kinase) #status exper
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase)
                                                                                                                                                                                                                                                                schwannomin - mouse (fragment)
schwannomin - mouse (fragment)
C.Species Mus musculus (fouse mouse)
C.Species Mus musculus (fouse mouse)
C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C.Accession: 154357
Hum. Mol. Genet. 3, 1075-1079, 1994
A,Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are A,Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are A,Reference number: 154357; MUID:95072570; PMID:7981675
A,Reference number: 154357
A,Reference number: 154357
A,Reference number: 154357
A,Reference number: 154367
A,Reference
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A;Cross-references: GB:L28838; NID:g454836; PIDN:AAA57150.1; PID:g601923
C;Genetics:
A;Gene: NF2
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26.2%; Score 11; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0;
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R;Horvath, A.; Kastin, A.J.
L; Biol. Coffen. 264, 2175-2179, 1989
A;Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor A;Reference number: A32039; MUID:89123285; PMID:2563371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Accession: S08606
R. Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
R. Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.
BENDO J. 5, 891-897, 1986
A; Ittle: The chicken osetrogen receptor sequence: homology with v-erbA and the human ose
A; Reference number: S07192; MUID:86247578; PMID:3755102
A; Recession: S08606
                                                  C;Accession: 167345

Kp. Cipaction 167345

Kp. Cipaction: 167345

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A;Reference number: 153243; MUID:86247587; PMID:3013627
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C.Species: Gallus gallus (chicken)
C.Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
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MHC H2-K-k cell surface glycoprotein - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
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A, Molecule type: mRNA
A, Residues: 1-7 < KRNA
A, Cross-references: EMBL:X03805, NID:g63378; PIDN:CAA27432.1; PID:g584490
C, Superfamily: unassigned leader peptides
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A;Aocession: Datein
A;Molecule type: protein
A;Residues: 1-4 - (4KOx-)
A;Experimental source: brain
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end
F;4/Modified site: amidated carboxyl end (Gly) #status experimental
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C;Keywords: glycoprotein
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seed protein ws-5 - winged bean (fragment)
c;Species: Psophocarpus tetragonolobus (winged bean)
c;Species: Psophocarpus tetragonolobus (winged bean)
c;Date: 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 07-0ct-1994
C;Accession: E61491
R;Hirano, H.
R;Hirano, H.
A;Title: Microsequence analyais of winged bean seed proteins electroblotted from two-dim A;Reference number: A61491; MUD:89351606; PMID:2765119
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A;Residues: 1-6 <RES>
A;Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829
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26.2%; Score 11; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels
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Job time : 20 secs
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A,Molecule type: protein
A,Residues: 1-7 <HIR>
C,Keywords: glycoprotein; seed
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3 STC 5
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March 8, 2004, 12:21:13 ; Search time 11 Seconds (without alignments) 33.136 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SwissProt_42:*

Database :

	Description	litoria			pachymed	mytilus	litoria	litoria	mytilus	_	-	н	e			pinu													-			litoria r	371	P41875 panagrellus
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16.7 16.7 16.7 16.7 16.7 16.7 16.7 11.9 11.9 11.9 11.9 11.9 11.9 11.9		LITRU EIII LITRU STA	P82096; 28-FEB-2003 (Rel. 28-FEB-2003 (Rel. 10-OCT-2003 (Rel.	Electrin 1. Litoria rubella (Desert tree f Litoria rubella (Desert tree f Eukaryota; Metazoa; Chordata; Amphibla; Batrachia; Anura; Ne Pelodryadinae; Litoria.	SEQUENCE. TISSUB-skin secretion; TISSUB-skin secretion; Wabnitz P.A., Bowie J.H., Tyler M.J "Peptides from the skin glands of ti Litori alectrica. Comparison with ti	rubella."; Aust. J. Chem. 52:639-645 (1999)	Query Match Best Local Similarity Matches 2; Conser	2 VPL 4 : 2 VPI 4	PESULT 2 VP19 HSV1K TP HSV1K TP HSV1B NC P212T0; DT 01-NOV-1991 (Rel. 20, Lel) DT 15-NAR-2004 (Rel. 43, Lel) DE Capsid assembly and DNA Capsid assembly and DNA Capsid protein VP19C) GN UL38 CAPSING SIMPLEX VITUSES, VITUSES; GBDNA VITUSES, OC Alphaherpesvirinae; Simplex VITUSES, OC Alphaherpesvirinae; Simplex VITUSES, NCBI_TAXID=10306; RN [1] RN [1] RN SEQUENCE FROM N.A. REDIINE=91101287; PubMee RN SILVERESSIMENT, Paparases RA SILVERESSIMENT, PAPAR
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-: SUBCELLULAR LOCATION: Secreted.
-: TISSUE SPECIFICITY: Skin.
-: HASS SPECIRCHETRY: MAE 699. 2; METHOD=MALDI.
-: MASS SPECIRCHETRY: MASS MIDATION.
-: MASS SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;
                                                                                                                            SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
                                                                                                                                                                                                                                                 -!- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.
                                                                                                                                                                      TISSUB-Skin secretion;
Chen T.B., Orr D.F., Shaw C.;
"Pachymedusa dacnicolor trypcophyllin-1 (PdT-1): structural
"Pachymedusa dacnicolor trypcophyllin-1 (PdT-1): structural
              Tryptophyllin-1 (PdT-1).
Pachymedusa dacnicolor (Giant mexican leaf frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Phyllomedusinae; Pachymedusa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.2%; Score 11; DB 1; Length 7; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=95380343; PubMed=7651886;
Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
Grauwels L., van Leuven F., de Loof A.;
"Identification, characterization, and immunological localization of
"Identification, characterization, and immunological beetle,
a novel myotropic neuropeptide in the Colorado potato beetle,
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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          expression of UL36, a true late gene involved in capsid assembly."; J. Virol. 65:769-786(1991).
-!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE EMBEDDED. BINDS DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leptinotaraa decemlineara.";
Peptides 16:365-374(1995).
-!- FUNCTION: Myotropic peptide. Stimulates the contractions of
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Myotropic neuropeptide | (Led-NNP-1).
Leptinotarsa decemineata (Colorado potato beetle).
Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
Chrysomelini; Leptinotarsa.
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                                                                              -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
                                                                                                                                                                                                                                                                                                                                26.2%; Score 11; DB 1; Length 6; 100.0%; Pred. No. 1.4e+05; tive 0; Mismatches 0; Indels
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SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
                                                                                                                                                                                                                                                                                               6 AA; 703 MW; 67376451A336F000 CRC64;
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(Rel. 41, Last sequence update)
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28-FEB-2003
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TPFY_PACDA
ID TPFY_PACDA
AC P83455;
DT 28-FEB-2003
DT 28-FEB-2003
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MNP1_LEPDE
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"Catch.":
"Catch.":
"Catch.":
"Catch.":
"Catch.":
"Catch.":
"I brain Res. 422:374-376(1987)
"I brain Res. 422:374-376(1987)
"I provertion: This peptide exhibits both potentiating (contraction)
and inhibitory (relaxation) effects on the anterior byssus
retractor muscle.

PIR, A2942; ECMUCR.

HORMODE, Amidation.

MOD_RES.

7 AMIDATION.
                        01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
01-MAR-1989 (Rel. 10, Last annotation update)
Catch-relaxing peptide (CARP).
Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TAXID=6550;
                                                                                                                                                                                                                                                                                                                                                                 Hirata I., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
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Similarity 33.3%; Pred. No. 1.40+05;
1; Conservative 2; Mismatches 0; Indels
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7 AA; 831 MW; 6734072687669DB0 CRC64;
7 AA
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6 AA.

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TISSUE-Pedal ganglion;
MEDLINE-88240357; PubMeda3377776;
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
"Structures and actions of Mytilus inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
--- FUNCTION: Inhibitory action on contractions in several molluscan
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Pedal ganglion;
MEDLINE-88240357; PubMed=3377776;
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.
"Structures and actions of Mytlius inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
--- FUNCTION: Inhibitory action on contractions in several molluscan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Contraction-inhibiting peptide II (MIP II).
Mytilus edulis (Houe mussel).
Bukaryota, Metazoa, Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Contraction-inhibiting peptide I (MIP I).
Mytilus edulis (Blue mussel).
Mytilus edulis (Blue mussel).
Mytiloidea; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 9; DB 1; Length 6;
Pred, No. 1.4e+05;
1; Mismatches 0; Indels
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6 AA; 637 MW; 72C9C68775B81000 CRC64;
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50.0%; Pred
1; W
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-!- SIMILARITY: TO MIP II.
PIR; A27696; A27696.
Hormone; Amidation.
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Hormone; Amidation.
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                                                                                                                                    CIP1 MYTED
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                                                                                                                                                                                                                                                                                                                                                        TISSUE-SKIN secretion;

A Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,

A Tyler M.J., Wallace J.C.,

A Tyler M.J., Wallace J.C.,

Tyler M.J., Wallace J.C.,

Titoria rubella'. The skin peptide profile as a probe for the study

T. Litoria rubella'. The skin peptide profile as a probe for the study

of evolutionary trends of amphibians.";

Aust. J. Chem. 49:955-963(1996).

-!- FUNCTION: May act as a neuromodulator or neurotransmitter.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCELLULAR LOCATION: Secreted.

-!- MASS SPECTROMETRY: MW-955; METHOD=FAB.

MAPPHIBIA defense peptide, Amidation; Neuropeptide;

MPTYCOLIGONE Carboxylic acid.

PYTYCOLIGONE CARDOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
"Peptides from the skin glands of the skin peptides from Litoria electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Litoria rubella (Desert tree frog).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                         Tryptophyllin 5.1.
Litoria ruballa (Desert tree frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae;
Pelodryadinae, Litoria.
NCBI_TAXID=104895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 10; DB 1; Length 7; Pred. No. 1.4e+05; 1; Mismatches 0; Indels
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SEQÜENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;
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7 AA; 983 MW; 7401E9D3676046B0 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                      7 AA.
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.8%; 50.0%;
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Best Local Similarity
Matches 1; Conserv
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2 IP 3
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ID EI03 LITRU
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SEQUENCE
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         RESULT 6
TYS1_LITRU
ID _TYS1_LIT
AC P82065;
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6 AA.

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19.0%;
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                                                                                                                                                                                                                                                                     Local Similarity 33.3
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=P.americana;
diaminononanoate.
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1 MTT 3
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P01373;
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Matches
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Shivan D., Campbell A.;
"Transcriptional regulation and gene arrangement of Escherichia coli,
Citrobacter freundii and Salmonella typhimurium biotin operons.";
                                                                                                                                                                                                                                                    A movel post-translational modification involving bromination of tryptophan. Identification of the residue, L-6-bromotryptophan, in peptides from Conus imperialis and Conus radiatus venom."; 2 Biol. Chem. 272:4689-4638 [197].

-!- FUNCTION: Does not elicit gross behavioral symptoms when injected centrally or peripherally in mice.

-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- MASS SPECIFICITY: Expressed by mETHOD=LSIMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-COT-2001 (Rel. 40, Last annotation update)
Adenosylmethionine 8-mnino-7-oxononanoate aminotransferase
(RC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
                                                                                                                                                                                                              MEDLINE=97184108; PubMed=9030520;
Craig A.G., Jimenez B.C., Dykert J., Nielsen D.B., Gulyas J.,
Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
McIntosh J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbecconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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Bromination; Amidation; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                            795 MW; 6EA37DC6D87EA6B0 CRC64;
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                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bromoheptapeptide Im.
                                                            7 AA.
                                                                                                                                                                                         SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION
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                                                                                                                             Conus imperialis (Imperial cone).
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                                                              STANDARD;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA;
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BRHP CONIM
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MOD RES
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                                          RESULT 10
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=76074708; PubMed=576;
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
-!- COFACTOR: Pyridoxal phosphate.
-!- PATHWAY: Biotin blosynthesis.
-!- STRUNTY: Mondimer.
-!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent aminotransferases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIES-P. americana; MEDLINE-81225865; PubMed-6113690; O'Shea M., Adams M.E.; Pubmed M.E.; Pertrapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shabanowitz J.; algoritolin in the central nervous system of the "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Periplaneta americana (American cockroach), and Limilus polyphemus (Atlantic horseshoe crab), and Carcinus maenas (Common shore crab) (Green crab). Bukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Prerygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattaria; Blattoidea; MCBI_TaxID=6978, 6850, 6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=L.polyphemus;
BEDLIME=90287800; PubMed=2356151;
Groome J.R., Tillinghast B.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 8; DB 1; Length 5;
Pred. No. 1.4e+05;
2; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005814; Aminotrans 3. PARTIAL. PROSITE; PS00600; AA TRANSFER_CLASS 3; PARTIAL. Biotin biosynthesis; Transferase; Aminotransferase; Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON TER 5 5 SEQUENCE 5 AA; 582 MW; GAAABIBIAGF00000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JU-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 A.A.
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PIR; 140697; 140697.
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PIR; A25269; A25269.
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       2 VP 3
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5 LP 6
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ID UNO6 PINPS
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                                                                                                                                                                                                                                                                                                                                                                                          SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAM373."
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                                                                                                                    RESULT 14
CIA BINTE
CIA BINTE
CIA BINTE
DD 01100
DT 01-000
DT 01-0
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01-JUN-1994 (Rel. 29, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
HTH-type transcriptional regulator trpl (TrpBA operon transcriptional activator) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                          Stangier J., Dircksen H., Keller R.;
"Identification and immunocytochemical localization of proctolin in pericardial organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).
-!-FUNCTION: Stimulates cardiac output and hindgut motility, modulates visceral and skeletal muscle in many arthropods.
-!- TISSUE SPECIFICITY: Found in the lateral white neurons and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  putida.";
Biochimie 71:521-531(1989).
Biochimie TI:521-531(1989).
FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGIYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRPAB OPERROM, OVERLAPPING ITS OWN PROMOTER REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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PROSITE; PS50931; HTH LYSR; PARTIAL.
Tryptophan biosynthesis; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                  19.0%; Score 8; DB 1; Length 5; 50.0%; Pred. No. 1.4e+05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.0%; Score 8; DB 1; Length 6; 50.0%; Pred. No. 1.4e+05;
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                                                                                                                                                                                                                                                                                                                             5 AA; 649 MW; 71B7673B44600000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PPG1 CIS;
MEDLINE=89335826; PubMed=2503057;
Eberly L., Crawford I.P.;
                                                            MEDLINE=86232789; PubMed=2872661;
                                                                                                                                                                                                                                    the crab pericardial organs.
PIR, A01644; HONOHA.
PIR; A60411; A60411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X13299; CAA31660.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                      1; Conservative
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 VP 3
                                                                                                                                                                                                                                                                                                             Neuropeptide.
SEQUENCE 5 1
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SEQUENCE
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[4]
SEOUENCE.
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TRPI_PSEPU
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                  01-07-1989 (Rel. 12, Created)
01-07-1989 (Rel. 12, Last sequence update)
01-07-1989 (Rel. 17, Last sequence update)
01-FBB-1991 (Rel. 17, Last annotation update)
Sex pheromone cAM373 (Clumping-inducing agent)
Enterococcus faecalia (Streptococcus faecalis).
Bacteria, Flinicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                              MEDLINE-87005252; PubMed=3093276;
Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
White B.A., An F.Y., Clewell D.B., Suzuki A.;
Isolation and structure of the Streptococcus faecalis sex pheromone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBL_TaxID=71647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Needle;
MEDLINE=99274088; PubMed=10344291;
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins.";
Blectrophoresis 20:1098-1108(1999).
-I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 6.6, its MM is: 25 kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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-!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS HARBORING PAM373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Uhrnown protein from 2D-page of needles (N141) (Fragment).
Pinus pinaster (Maritime pine).
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Similarity 50.0%; Pred. No. 1.4e+05;
1; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lett. 206:69-72(1986)
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Best Local Similarity 66.73
Matches 2, Conservative
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   STANDARD;
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Matches 1; Conservat
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Gaps

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0; Indels

1; Mismatches

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Search completed: March 8, 2004, 12:29:51 Job time: 12 secs

human adeno human adeno human adeno

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sphingomona lactobacill

bionectria caenorhabdi amblyopyrum hordeum vul peridictyon aegilops ta bromus iner pseudoroegn

lophopyrum

Q9YVE3
Q9YIR9
Q9YIRQ9
Q9YIRQ9
Q8JJ20
Q6568
Q47029
034028
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092214
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hordeum bra henrardia p agropyron c

spinacia ol

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thinopyrum australopyr heteranthel

haynaldia v taeniatheru hordeum mar

P92442 P92226 P92385 P92421

ALIGNMENTS

crithopsis

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
C-terminus of the viral replicase (Fragment).
Cherry leaf roll virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-96124520; PubMed-8560786;
Borla M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
Borla M., Sanchez F., Rowhani A., Bruening at the 3' terminal "Lorg, nearly identical untranslated sequences at the 3' terminal regions of the genomic RNAs of cherry leafroll virus (walnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borja M.;
Themis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.5%; Score 17; DB 12; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strain).";
Virus Genes 10:245-252(1995).
EMBL; 234265; CAA84019.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=12615;
                                                                                          CIP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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P70804 azotobacter
P72081 nocardia la
Q89112 borrelia bu
Q965b3 arabidopsis
Q07624 rous sarcom
P83569 sepia offic
C50556 actinobacil
Q544848 trreptomyce
O55184 rattus norv
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O42564 fugu rubrip
P83308 gallus gall
Q67113 influenzavi
Q67113 homo sapien
Q8mh77 taraxacum (
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                                                                                                                                                                              March 8, 2004, 12:26:58; Search time 39 Seconds (without alignments) 56.631 Million cell updates/sec
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SEQUENCE FROM N.A.
MEDLINE-81001892; PubMed=7407922;
MEDLINE-81001892; PubMed=7407922;
MEDLINE-810101892; PubMed=7407922;
"Nonviral oligonuclectides at the 5' terminus of cytoplasmic influenza viral mRNA deduced from cloned complete genomic sequences.";
viral mRNA deduced from cloned complete genomic sequences.";
EMEL; MAS045; AAA43202.1;
NON_TER
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Malakooti J., Ramaswamy K.;
Malakooti J., Ramaswamy K.;
Milecular cloning and characterization of the human Na+/H+ exchanger wholecular cloning and characterization of the human NHE-3 gene promoter region.";
Submitted (UNN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282824; AAM53436.1;
SEQUENCE 7 AA; 842 MW; 74072DQ772D406F0 CRC64;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3'
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(TrEMBLrel. 24, I
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Matches 2; Conservative
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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pubMed=613771;
pubMed=613771;
Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
"A novel active pentapeptide from chicken brain identified by
antibodies to FWRFamide.";
Nature 305:328-330 (1983);
-!- FUNCTION: MAY FONCTION AS A NEUROTRANSMITTER OR MODULATOR.
-!- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PREFIDE)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha; Tetradotoidea, Tetraodontidae,
NCBI_TaxID=31033;
                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 24, Last annotation update)
01-JAN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
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Pred. No. 1e+06;
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5 AA; 645 MW; 69D4073767400000 CRC64;
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        7 AA.
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GO; GO:0005216; F:ion channel activity; IEA
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Gallus gallus (Chicken).
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EMBL: Z21682; CAA79797.1; -.
                                                                                                                                                                                                           Rehm B.H.A., Ertesval H., Valla S.;
Rehm B.H.A., Ertesval H., Valla S.;
"A new Azotobacter vinelandi; mannuronan C-5-epimerase gene (algG) is part of an alg gene cluster physically organized in a manner similar to that in Pseudomonas aeruginosa.",
J. Bacteriol. 178:5884-5889(1996).
J. Bacteriol. 78:5884-5899(1996).
NON TER 1
SEQÜENCE 7 AA, 684 MW; 71B5A5A5A2D1AED0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE=96009872; PubMed=7557411;
Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
Lizas P.;
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0
                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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0
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Last sequence update)
Last annotation update)
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3'-methylcephem hydroxylase (Fragment)
                                                                                                                                                                                  STRAIN=E;
MEDLINE=96427318; PubMed=8830682;
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23,
24,
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Similarity 33.3%;
2; Conservative 1
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Best Local Similarity 66.7
Matches 2; Conservative
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                                                                                    Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nocardia lactamdurans.
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                    NCBI_TaxID=354;
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01-MAR-2003 (
01-JUN-2003 (
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EMBL, U75692, AAC49682.1; -.
GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
GO; GO:0016829; F:1yase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon esculentum (Tomato).

Bukaryote, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Lamiids; Solanales; Solanaceae; Solanum.

NCBI_TaxID=4081;
                                                              Chloroplast.

Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, asterids;
campanulids, Asterales; Asteraceae; Cichorioideae; Cichorieae;
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Octiker J.H., Olson D.C., Shiu O.Y., Yang S.F.; nifferential induction of seven 1-aminocyclopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato (Incoparsion esculentum).";
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                    "Reconstruction of the evolution of trnP pseudogenes."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AV01647; AAK21591.1: --
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1 7 AA; 828 MW; 71B412C7377415D0 CRC64;
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7 AA; 675 MW; 687451B5A76DDB70 CRC64;
                                                                                                                                                                                                                                                                                                                                             26.2%; Score 11; DB 8;
50.0%; Pred. No. 1e+06;
iive 1; Mismatches
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                                              (sect. Dioszegia) sp. 4310Hnew.
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Matches 2, Conservative
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Best Local Similarity
                                                                                                                                          NCBI_TaxID=154248;
                                                                                                                                                                           SEQUENCE FROM N.A.
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                   PsbA (Fragment)
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LE-ACS1B.
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NON TER
SEQUENCE
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P70804;
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Matches
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-1. DEVELOPMENTAL STAGE: FIRST APPEARS IN THE OVARIAN FOLLICLES FURING VITELLOGENESIS. ACCUMULATES IN THE COCYTES BEFORE BEING SECRETED DURING FREFILIZATION. EXPRESSION CONTINUES IN THE EMBEDDED COCYTE. ACCUMULATES IN THE EGG CAPSULE AFTER FERTILIZATION.
-1. MASS SPECTROMETRY: NW=596.6; METHOD=MALDI.
                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF SEQUENCE OF The open reading frames of Rous sarcoma virus leader RNA in translation and genome packaging.";
EMBO J. 11:3747-3757(1992).
EMBI, X67581; CAA47862.1;
SEMBI, X6758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Separm attracting peptide SepSAP.
Sepia officinalis (Common cuttlefish).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Decapodiformes; Sepioidea; Sepiidae; Sepiia.
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Biochem. Biophys. Res. Commun. 296:1186-1193(2002).
-!- FUNCTION: ATTRACTS SPERM INCREASING THE CHANCES OF GAMETE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zatylny C., Marvin L., Gagnon J., Henry J.; "Pertilization in Sepia officinalis: the first mollusk sperm-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Rous sarcoma virus (strain Prague C).
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
NCBI_TaxID=11888;
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Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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6 AA; 597 MW; 72C8676AA0470000 CRC64;
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01-0TN-1998 (TrEMBLrel. 06, Last sequence update)
01-0TN-2001 (TrEMBLrel. 17, Last annotation update GlyA (Fragment).
Actinobacillus actinomycetemcomitans (Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 9; DB 5;
Pred. No. 1e+06;
1; Mismatches
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50.0%;
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Matches 1; Conservative
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PubMed=12207899;
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1D 05055
AC 05055
DT 01-JU
DT 01-JU
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ON GLYA.
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                                                                                                                                                                                                             Stevenson B., Miller J.C., "Comparative analyses of Borrelia burgdorferi erp genes and their cp32 prophages: conservation amidst diversity."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                       Plasmid group cp32-9.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBL_TaxID=139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUBE-Root;
MEDLINE-21025; PubMed=11277426;
MEDLINE-2117.025; PubMed=11277426;
MEDLINE-2117.025; PubMed=11277426;
MATADIDOPSIS thaliana genes expressed in the early compatible interacion with root-knot mematcodes.";
MOI. Plant MICTOBE Interact. 14:288-299(2001).
EMBL; AJ286350; CAB71014.2; --
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
UORF1.
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Last annotation update)
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                                                                  Borrelia burgdorferi (Lyme disease spirochete).
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                                                                                                                                                                                                                                                                                            EMBL; AY142100; AAN17911.1; -. GO; GO:0046821; C:extrachromosomal DNA; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0TN-2001 (TrEMBLrel. 17, Created) 01-0TN-2001 (TrEMBLrel. 17, Last sequel-01-0CT-2003 (TrEMBLrel. 25, Last annu Hypothetical protein (Fragment). DIDI 10A-2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                           PF-50 protein (Fragment). PF-50.
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Best Local Similarity
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SEQUENCE
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Q07624
ID Q0762-
AC Q0762-
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Q9C5B3
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STRAIN=N2-3-11;

RX MEDLINE=20011291; PubMed=10542330;

RX MEDLINE=20011291; PubMed=10542330;

RA Poshling S., Piepersberg W., Mehmeist U.F.;

RA Poshling S., Piepersberg W., Mehmeist U.F.;

RI N2-3-11 and interaction of the SecY protein with the SecA protein.";

RI N2-3-11 and interaction of the SecY protein with the SecA protein.";

RI N2-3-11 and interaction of the SecY protein with the SecA protein.";

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                                                                                                                                                                                                   Kraig E.;
"cis Elements and trans factors are both important in strain-specific regulation of the leukotoxin gene in Actinobacillus actinomycetemcomitans.";
Infect. Immun. 64:3451-3460(1996).
EMBL; US1862; AAB88721.1;
                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN-AICC 33384;
MEDLINE-96355846; PubMed=8751884;
Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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0
           Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Actinobacillus.
NCBL TaxID=714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces griseus.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Streptomycinese, Streptomycinese, Streptomycines.
NCBI_TaxID=1911;
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21.4%; Score 9; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
21.4%; Score 9; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;
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actinomycetemcomitans).
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1 VTVT 4
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3 LPV 5
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Q54248;
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Q54248
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Search completed: March 8, 2004, 12:30:43 Job time : 40 secs

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March 8, 2004, 12:20:28; Search time 52 Seconds (without alignments) 38.035 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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geneseqp20028:*
geneseqp2003a8:*
geneseqp2003bs:*
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1 CVPLTSC 7
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aau04530 VEGF base		~	<u></u>	4	Kidney			₽	œ	_	_		-	-		Cadher		٠,	_		_	_		Aay63236 Protocadh	
SUMMARIES	E	4 AAU04530	2 AAW13421	3 AAB12007	4 AAE11813	5 AAU10724	6 ABU59533	7 ADC33700	7 ADC33699	4 AAU04531	5 ABJ00550	5 ABG33862	3 AAY61489	3 AAY62764	3 AAY62007	3 AAY62224		3 AAY64260	2 AAR51449			3 AAY62758	3 AAY64322	3 AAY61506	3 AAY62489	3 AAY63236	
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

Claim 49; Page 32; 102pp; English.

	Aar15772 Farnesyl-	Aar49769 Farnesylt	Vacured February			Aaw67428 HCV pepti	nris7236 Rhodonsin				Aaw67430 HCV pepti	This office Tours		_	Aay62135 Cadherin-	Aave 3266 Protocadh			Abj04536 Molt-4 le	Aaw60386 Tumour ho	and memili C1750c.		Aabu3612 Aspergill	Aav64262 Cadherin-	
7 S ABB47076	4 2 AAR15772	09107044 C 7	2 PARA 2 4	4 2 AAR77833	4 2 AAW04459	E 2 ANG 7428	OTT COLUMN 7 C	_	7 2 AAR36871	7 2 AAR43615	0c873W64 C C	2 AAMO1430	7 3 AAY64307	7 3 AAY64292	7 2 AAVE2125	CONTRACTOR OF T	7 3 AAY63266	7 5 ABB46174	7 5 ABJ04536	7 2 22 28 6	COCONIUM 7	7 2 AAW93712	7 3 BARN3612		7 3 AAY64262
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ALIGNMENTS

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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                               Human, VBGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                             1. .7
/note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                  Cendron A;
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Stacker S,
AAU04530 standard; peptide; 7 AA.
                                                                 VEGF based monocyclic peptide 8.
                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                           18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                      18-JAN-2001; 2001WO-US001533.
                                            (first entry)
                                                                                                                                                                                                                                                                                                                                   Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442248/47.
                                                                                                                                                                     Key
Disulfide-bond
                                                                                                                                                                                                               WO200152875-A1
                                                                                                                                                                                                                                     26-JUL-2001.
                                              26-SEP-2001
                                                                                                                                               Synthetic.
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                         AAU04530;
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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, che condition is diabetic retinopathy, psoriasis, arthropathy, che condition is diabetic retinopathy, psoriasis, arthropathy, chemanjoina, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenois, head, heat or cold cramma, substance induced neovascularised malignant of the liver, excessive cramma, substance induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability cor brain. The peptides are also used to image blood vesels and lymphatic or brain. The peptides are used to image blood vesels and lymphatic or brain. The peptides are used to image blood vesels and lymphatic cor vasculature. The monomeric and bicyclic peptides are used to interfere control inflammation, especially rheumatory agent, to treat a cordinary corticular inflammation, especially rheumatoid arthritis, psoriasis and dishard corticulariants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This synthetic peptide is a claimed example of a kidney-homing peptide that was identified using a novel method for obtaining molecules that home to a selected organ or tissue. This in vivo panning method typically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obtaining compound that homes to selected organ or tissue - by in vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kidney homing peptide; in vivo panning; screening; phage display;
drug delivery.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 42; DB 4; Length 7; ; Pred. No. 1.4e+06; 0; Mismatches 0; Indel8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW13421 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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95US-00526710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 100.7; Conservative
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a mouse kidney homing peptide. This sequence was identified by using in vivo panning to screen a library of potential organ homing molecules. The present sequence can be used to direct a molety to a kidney tissue, by linking the molety to the present sequence. Examples of potential moleties are drugs, toxins or a detectable label
                                                                                                                                                                                                           ..
0
involves administering a phage display library to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see AAW13412-52, AAW1181-86) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly identified in vivo, as compared to prior art in vitro screening methods, which require further examination to see if they maintain specificity in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kidney; homing peptide; organ targeting; tissue targeting; mouse; cyclic.
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                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                 Score 31; DB 2; I
Pred. No. 1.4e+06;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Col 18; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                 AAB12007 standard; peptide; 7 AA.
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57.1%;
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97US-00813273.
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                                                                                                                                                                                        73.8%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruoslahti E;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kidney homing peptide # 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BURN-) BURNHAM INST.
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Best Local Similarity
                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                              1 CVPLTSC 7
                                                                                                                                                                                                                                                                           CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasqualini R,
                                                                                                                                                           Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-SEP-1995;
10-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                             17-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6068829-A.
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                                                                                                                                                                                                                                                                                                                                                                                AAB12007;
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                                                                                                                                                                                                                                                                                                                          RESULT 3
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1 CVPLTSC 7

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95US-00526710. 97US-00813273. 97US-00862855.

99US-00227906.

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Organ targeting; tissue targeting; cancer; tumour homing molecule; delivery of target molecule; kidney homing peptide.
 Kidney homing peptide #1 useful for delivery of target molecules.
                                                                                                                                                                                                   Ruoslahti E, Pasqualini R;
                                                                                                                                                                              (BURN-) BURNHAM INST.
                                                                                                                    08-JAN-1999;
                                                                                                                                                             23-JUN-1997;
                                                                             US6306365-B1
                                                                                                                                         11-SEP-1995;
                                                                                                                                                    10-MAR-1997;
                                                                                                 23-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU59533;
                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an enriched library fraction containing molecules that selectively home to a selected organ or tissue such as brain, kidney or tumour recovered by in vivo panning. The invention generally relates to the field of molecular medicine, drug delivery and to a method of invivo panning for identifying a molecule that homes to a specific organ. The molecules, e.g., peptides, peptidomimetics, proteins and fragments of proteins contained in an enriched library fraction may be administered to a subject as part of a pharmaceutical composition to from bacteriophage targetted to kidney. (Updated on 11-SEP-2003 to
                                                                                                                                                                                                                                                                                                                                                                               Enriched library fraction comprising molecules recovered by in vivo panning that selectively home to a selected organ or tissue useful for treating disease or in diagnostic methods.
                                                                                                                                                      Enriched library fraction; brain; kidney; tumour; panning; diagnostic; molecular medicine; drug delivery; peptidomimetic; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.8%; Score 31; DB 4; Length 7; 57.1%; Pred. No. 1.4e+06; ive 2; Mismatches 1; Indels
                                                                                                                                   Phage peptide #21 targetted to kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU10724 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Col 18; 21pp; English.
                                                               AAE11813 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                 95US-00526710.
                                                                                                                                                                                                                                                                                           97US-00813273.
                                                                                                                                                                                                                                                             99US-00226985.
                                                                                                                                                                                                                                                                                                                                            Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                        unidentified bacteriophage
                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                        (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standardise OS field)
                                                                                                                                                                                                                                                                                                                          (BURN-) BURNHAM INST.
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CLPVASC '
     |:|: ||
1 CLPVASC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                              Ruoslahti E,
                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                       US6296832-B1
                                                                                                                                                                                                                                                               08-JAN-1999;
                                                                                                                                                                                                                                                                                                       23-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                 11-SEP-1995;
                                                                                                                                                                                                                                                                                             10-MAR-1997;
                                                                                                         11-SEP-2003
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Best Local Si
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                                                                                     AAE11813;
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ID AAU1
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AC AAU1
XX
DT 12-N
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                                               RESULT 4
                                                         AAE11813
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The present invention relates to a method of recovering molecules that the present invention relates to a method comprises administering to home to a selected organ or tissue. The method comprises administering to the subject the library of diverse molecules, collecting a sample of the calcadorgan or tissue (e.g. brain or kidney), and recovering from the sample everal molecules that home to the selected organ or tissue. The cample study of the control of the selected organ or tissue. The careening large number of molecules (e.g. peptides), that home to specific organ. The identified molecule is useful for e.g. raising an careening large number of molecules (e.g. peptides), that home to a target molecule, targeting a desired moiety (e.g. antibody specific for a target molecule, targeting a desired moiety (e.g. careing is useful for identifying the presence of cancer in a subject by company to a selected organ and, therefore provides a sugnificant advantage over previous methods, which require that a subject complementation is a subject of a selected organ and, therefore provides a significant advantage over previous methods, which require that a subject of subject identified using an in vitro screening method subsequently be considered to determine if it maintains its specificity in vivo. AAU10724-
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                                                         Recovering molecules that home to an organ or tissue, useful for identifying molecules that home to a specific organ or tissue, e.g. identifying a tumor homing molecule to identify the presence of cancer, by in vivo panning of a library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kidney receptor targeting peptide #1.
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                                                                                                                                                                                                                                                                                          Example 2; Col 18; 21pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
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CLPVASC 7
WPI; 2002-040196/05.
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Best Local Similarity
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Synthetic.

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18-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a composition comprising a bioactive agent commogeneously dispersed in a targeted matrix (polymer and targeting homogeneously dispersed in a targeted matrix for use as a delivery ligand). Also included are a targeted matrix for use as a delivery convention in the bioavailability of an agent comprising administration of the composition and treating cancer comprising administration of the composition. The method is useful for targeted delivery of a drug, capecially in cancer therapy. The targeting ligand may be a peptide. Examples of targeting peptides targeting receptors in the brain and kidney, considerate peptides, peptides targeting receptors in the brain and kidney, peptides targeting the RGD (Arg-Gly-Asp) motif in, e.g., antibodies, peptides angiogenic endothelium of solid tumours, tissue specific peptides (e.g. of lung, skin, pancreas, intestine, uterus, adrenal gland and retina), and cationic cancer-targeting peptides. The present sequence is a peptide targeting ligand disclosed in the invention
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                                                                                                                                                                                                                                                                                                                                                                                              Targeted delivery system comprising a bioactive agent homogeneously dispersed in a targeted matrix is especially useful in cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
 cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor; fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium; tumour; cationic cancer-targeting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chimeric retrovirus envelope protein; ecotropic envelope protein; cytostatic; gene therapy; cancer.
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                                                                                                                                                                                                                                                                                                                                    Ramaswami V, Romanowski MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kidney cell targeted peptide SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Page 38; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.8%; 57.1%;
                                                                                                                                                                                                                         2000US-00703474.
                                                                                                                                                                        25-JUL-2001; 2001US-00912609.
                                                                                                                                                                                                        )5-JAN-2000; 2000US-00478124
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                                                                                                                                                                                                                                                                                                                                         Matsunaga TO,
                                                                                                                                                                                                                                                      (UNGE/) UNGER E C.
(MATS/) MATSUNAGA T O.
(RAMA/) RAMASWAMI V.
(ROMA/) ROWANOWSKI M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                            US2002041898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7 AA;
                                                                                                                                                                                                                            31-OCT-2000;
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                                                                                                                                           11-APR-2002.
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Unger EC,

ADC33700;

RESULT 7

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the present inventiou describes a climatric frotovirus exercises conversely from the corporation and a heterologous short comprising an ecotropic envelope protein and a heterologous short described: (1) a nucleic acid molecule comprising a sequence encoding the described: (1) a nucleic acid molecule comprising a sequence encoding the comparison at the comprising a nucleic acid sequence encoding the chimeric envelope protein comprising a retroviral particle comprising a chimeric envelope protein comprising a retroviral particle comprising a chimeric envelope protein comprising a retroviral at alters viral tropism; (3) altering retroviral tropism; (4) identifying a nucleic acid sequence encoding the chimeric envelope protein comprising to be used in gene therapy. The chimeric retrovirus envelope protein is consecuted in gene therapy. The chimeric retrovirus envelope protein is consecuted in contraing cancer, which comprises providing a cancer cell, e.g. thuman cancer cell and infecting the cancer cell with a virus, e.g. thuman cancer cell and infecting the cancer cell with a virus, e.g. therefologous short peptide ligand and a therapeutically useful gene, e.g. therefore the chimeric envelope protein comprising a encoding thymidine kinase. The present sequence represents a kidney cell transfered peptide, which is given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                    New chimeric retrovirus envelope protein comprising an ecotropic envelope protein and a heterologous short peptide ligand inserted within the ecotropic envelope protein useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a chimeric retrovirus envelope protein (I) comprising an ecotropic envelope protein and a heterologous short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 4; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC33699 standard; peptide; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.8%;
57.1%;
07-MAR-2003; 2003WO-US007323.
                                                                             08-MAR-2002; 2002US-0362655P
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                                                                                                                                                       UYMA-) UNIV MASSACHUSETTS
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                                                                                                                                                                                                                                Gollan IJ;
                                                                                                                                                                                                                                                                                                  WPI; 2003-722332/68.
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Best Local Similarity
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CLPVASC
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                                                                                                                                                                        The present invention describes a chimaric retrovirus envelope protein (I) comprising an ecotropic envelope protein and a heterologous short peptide ligand inserted within the ecotropic envelope protein. Also peptide ligand inserted within the ecotropic envelope protein. Also cereombinant chimaric acid molecule comprising a sequence encoding the chimaric envelope protein; (3) a recombinant retroviral particle comprising a chimaric envelope protein; (3) a recombinant retroviral particle comprising a chimaric envelope protein comprising a nucleic comprising a chimaric envelope protein that alters viral tropism; (4) altering retroviral tropism; (4) chercilogous short peptide ligand; (3) altering retroviral tropism; (4) dentifying a nucleic acid sequence concerning the chimaric envelope protein is used in gene therapy. The chimaric retrovirus envelope protein is useful for treating cancer. (I) has cytostatic activity and cancer call and infecting the cancer cell with a virus, e.g. thuman cancer cell and infecting the cancer cell with a virus, e.g. chrowing thymidine kinase. The present sequence represents a kidney cell and any chimaric carporation of the present carpetide protein in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                     New chimeric retrovirus envelope protein comprising an ecotropic envelope protein and a heterologous short peptide ligand inserted within the ecotropic envelope protein useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neovascularisation; lymphangiogenešis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.8%; Score 31; DB 7; I 57.1%; Pred. No. 1.4e+06; iive 2; Mismatches 1;
                                                                                                                                                     Disclosure; SEQ ID NO 3; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04531 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEGF based monocyclic peptide 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
         UYMA-) UNIV MASSACHUSETTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                     Gollan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|: ||
CLPVASC 7
                                                                WPI; 2003-722332/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200152875-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU04531;
                                      Green MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04531
ID AAU
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vegen (vascular endothelial growth factor). The invention relates to a vegen (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-copy peptide loop fragment from an exposed loop of a growth factor protein and peptides (included loop fragment from an exposed loop of a growth factor protein and peptides dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior copyclisation are used to interfere with angiogenesis, to cyclisation are used to interfere with angiogenesis, condition or lymphangiogenesis, to cyclisation or lymphangiogenesis, to cyclisation or lymphangiogenesis.

CC characterised by angiogenic included neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, thead, heat or cold characterised by angiogenic analignant or benign tumour, post-recovery correlated angiogenic dysfunction, diabetes induced neovascular sequelae, incompre-related angiogenic dysfunction, diabetes induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal least one piological activity induced by VBGF, VBGF-C or D and correlation in peripheral limbs or in lungs, peritoneal cavity, pleura, a committion with an least one biological activity induced by VBGF, VBGF-C or D and chronic inflammation, especially rheumatoid arthritis, psoriasis and chronic inflammation, especially rheumatoid arthritis, psoriasis and chronic inflammation, especially rheumatoid arthritis, psoriasis and corrections and proper corrections and parthritis and and and activity induced by veget becomes or corrections and activity induced by VBGF, C or D and corrections and activity induced are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressive; nephrotropic; antirheumatic; antiarthritic; neuroprotective; cytostatic; immunostimulant; antiarthritic; antiaslergic; thyromimetic; antianaemic; haemostatic; dermatological; antiallammatory; cardiant; ophthalmological; uropathic; antidiabetic; antithyroid; antidepressant; hepatotropic.
                                                                                                                                                   Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B lymphocyte stimulator protein binding protein; BLyS; immune disease; allergy; proliferative disease; infectious disease; arteriosclerosis; inflammatory disorder; hypergammaglobulinaemia; blood clotting; ischaemia; graft-versus-host disease; neurodegenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B lymphocyte stimulator protein binding peptide #1.
Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ00550 standard; peptide; 7 AA.
    Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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              Hughes RA,
                                                                                               WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVPLT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2002
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              Achen MG,
                                                                                                                                                                                                                                                                                                                                         residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Unidentified

Ladner

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Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; CB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-12; cadherin-14; cadherin-15; T-cadherin, PB-cadherin; cadherin cadherin related neuronal receptor; LI-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                           New B-lymphocyte stimulator binding polypeptide useful in detecting or isolating BLyS or BLyS-like polypeptide comprises a specified amino acid
                                                                                                                                                                                               The invention relates to a B Lymphocyte Stimulator (BLyS) binding polypeptide. BLyS binding peptides bind BLyS or BLyS-like proteins reversibly or irreversibly. The binding peptides are used in detection, isolation and/or putification of BLyS in a solution such as water or a buffer solution, as well as any fluid and/or cell obtained from an individual biological fluid, body tissue, body cell, cell line, tissue culture or other source containing BLyS or BLyS-like polypeptides. The biological fluids sinclude sera, plasma, lymph, blood, blood fraction, urine, synovial fluid, spinal fluid, saliva and mucous. Sequences ABG33415, ABG33415, ABG33458-3386, ABG33859-3386, the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1375.
                                                                                                                                                                          Disclosure; Page 132; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                         Fleming TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY61489 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-00073040.
98US-00187859.
99US-00234395.
99US-00264516.
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                                                                                                                                                                                                                                                                                                                                                                                                                  66.7%;
57.1%;
18-AUG-2000; 2000US-0226489P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                           Potter MD,
                                                                                     WPI; 2002-351647/38.
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CXPXTGC 7
                               (DYAX-) DYAX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1998;
06-NOV-1998;
20-JAN-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0S-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ното варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000
                                                            Beltzer JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY61489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY61489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the treatment, prevention or amelioration of a disease or disorder associated with: aberrant B amelioration of a disease or disorder associated with: aberrant B cultivity of the complex origin; or proliferative disease; and reducing, inhibiting or stimulating immunoglobulin production, B cell proliferation inhibiting polypeptides are used in the treatment, prevention or the BryS binding polypeptides are used in the treatment, prevention or amelioration of diseases such as immune system diseases, proliferative diseases, diseases, answere cities of hematopoletic origin, graft rejection, hypergammaglobulinaemia, blood clotting disorders, inflammatory disorders, hypergammaglobulinaemia, blood clotting disorders, ischaemia, and neurodegenerative diseases. The present sequence is a B lymphocyte stimulator protein binding peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B Lymphocyte Stimulator protein, B Lymphocyte Stimulator binding peptide;
BLyS; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
                                                                                                                                                                                                                                                                                                                   The treatment of various diseases e.g. rheumatoid arthritis, comprises administering B Lymphocyte stimulator binding polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B Lymphocyte Stimulator (BLyS) binding peptide #436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 5; L
Pred. No. 1.4e+06;
); Mismatches 3;
                                                                                                                                                                                                                                                              Rosen CA;
                                                       /label= Phe, Trp, Tyr
                                                                                                                                                                                                                                                                Fleming TL,
                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Claim 69; Page 233; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG33862 standard; peptide; 7 AA.
                                                                                     /label= Pro, Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLys; biological fluid; serum; synovial fluid; saliva; mucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-2001; 2001WO-US025891.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 66.7%;
Local Similarity 57.1%;
hes 4; Conservative (
                                                                                                                                                                                                        18-AUG-2000; 2000US-0226700P.
                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                          17-AUG-2001; 2001WO-US025850
                                                                                                                                                                                                                                                                 Potter DM,
                                                                                                                                                                                                                                                                                             WPI; 2002-499775/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CXPXTGC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200216412-A2
                                         Misc-difference
                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
                                                                                                                    WO200216411-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2002
                                                                                                                                                                                                                                                                   Beltzer JP,
                                                                                                                                                  28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG33862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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Gaps

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Score 28; DB 5; Length 7; Pred. No. 1.4e+06; 0; Mismatches 3; Indels

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11-NOV-1999
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                                                                                                                                                                                                                                                                                                                             The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion comprising peptides which comprise a nonclassical cadherin-mediated functions. They can be used for e.g. nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of a drug to a tumour in a mammal, treating cancer in a mammal, enhancing delivery of a drug to a tumour in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting conclassion closes and in a mammal, enhancing delivery to the cortral nervous system, treating apoptosis in a nonclassical cadherin-expression in a mammal, enhancing delivery to the conclassical cadherin-expressing cells, inhibiting synaptic stability in conclassical cadherin-expressing cells, inhibiting synaptic stability in conclassical cadherin-expressing cells, inhibiting synaptic stability in conclassical cadherin-expressing confirmed adhesion of foreign taste in a celecting scar tissue, or enhancing adhesion of foreign tissue in a conclassical modular degeneration, multiple solerosis and diabetes. The mammal. They can also be used for treating e.g. psoriasis, arthritis, age conclassing the process of the process and the process to the process the process in the process the process in the process and the process the process in the process and the process of the proces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..0
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                                                                                                                                                              New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PB-cadherin cell adhesion recognition cyclic peptide SEQ ID NO:4047.
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Pred. No. 1.4e+06;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                         Claim 36; Page 172; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY62764 standard; peptide; 7 AA.
           (ADHE-) ADHEREX TECHNOLOGIES INC
                                                                Gour BJ, Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.9%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                        WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CVPLTSC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY62764;
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The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion comprising peptides which comprise a nonclassical cadherin-mediated functions. They can be used for e.g. nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting certains of a cancer in a mammal, inhibiting concerning angiogenesis in a nonclassical cadherincer expressing cell, preventing or treating obesity in a mammal; stimulating contral nervous system, treating a demyelinating neurological disease, concrassing vasopermeability in a mammal, enhancing adhesin expressing cells, inhibiting synaptic stability in nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age corrected marchial adgeneration, multiple sclerosis and diabetes. The mammal and particular and diadetes; and an analy to AAX64572 represent specifically claimed peptides, and in AAX33183 to AAX66542 to AAX64572 represent specifically claimed peptides, and in AAX33186 represent sequences used in the contrast of the vector in the properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-17; cadherin-18; cadherin-12; cadherin-15; T-cadherin; PB-cadherin; cadherin-16; adherin related neuronal receptor; LI-cadherin; protocadherin; cadherin; desmocollin; calcium binding; cancer; tumour; obesity;
                                                                                                                                                                                                                                                                                                                                                                               New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 72; Page 193; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY62007 standard; peptide; 7 AA.
                                                                                                                                                                                                          (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                       Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.5%;
                                                                                                                99US-00234395.
99WO-CA000363
                                                         98US-00073040
                                                                                      98US-00187859
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                                                                                                                                                                                                                                                                           Gour BJ,
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                 WPI; 2000-038791/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 AA;
                                                                                                                                                                                                                                                                           Blaschuk OW,
   05-MAY-1999;
                                                                                          06-NOV-1998;
                                                                                                                       20-JAN-1999
                                                                                                                                                       08-MAR-1999;
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0;

W09957149-A2.

(first entry)

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New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                               Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin-16; T-cadherin; PB-cadherin; protocadherin; desmocollin; calclum binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                            Cadherin-14 cell adhesion recognition cyclic peptide SEQ ID NO:3971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blaschuk OW,
                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                  W09957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1999;
02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1999
                                                                                                                                                                                                                                                                          Synthetic
The present invention describes cadherin modulating agents (WA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating on nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, confiniting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting confined apoptosis in a mammal, simulating conformation of the contral nervous system, treating obesity in a mammal, stimulating contral nervous system, treating a demyelinating neurological disease, conclassical cadherin-expressing cells, inhibiting synaptic stability in nonclassical cadherin-expressing cells, inhibiting synaptic stability in conclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age con reducing cart tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age contract can also be used for detection and diagnosis and in bioreactors. Apy66592 to Apx64572 represent specifically claimed peptides, and conclassing cells invention and diagnosis and in bioreactors. Apx64573 to Apx64573 and Apx33183 to Apx33186 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cadherin modulating agents, used for modulating nonclassical cadherin -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
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    rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 3; Length 7; Pred. No. 1.4e+06; 0; Mismatches 3; Indel8
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 48; Page 180; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Byers S;
                                                                                                                                                                                                                                                                                                                          98US-00073040.
98US-00187859.
99US-00234395.
99US-00264516.
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                                                                                                                                                                                                                                                                                       99WO-CA000363.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-038791/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7 AA;
                                                                                                                                                           Disulfide-bond
                                                                                                  Homo sapiens.
                                                                                                                                                                                                    W09957149-A2
                                                                                                                                                                                                                                                                                     05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                 05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blaschuk OW,
                                                                                                                                                                                                                                                                                                                                                    06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1999;
                                                                                                                                                                                                                                              11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                        0-JAN-1999
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                                                                            Synthetic.
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Best Local S
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Byers S;

Gour BJ,

98US-00073040. 98US-00187859. 99US-00234395.

99WO-CA000363

99US-00264516.

Location/Qualifiers

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The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion comprising peptides which comprise a nonclassical cadherin real condition (CAR) sequence. The MAS can be used for endicated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug to a tumour in a mammal, irrating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting cancer in a mammal, inhibiting concerning apoptosis in a nonclassical cadhering or treating obesity in a mammal, stimulating contrain nervous system, treating a demyeliating delivery to the contral nervous system, treating a demyeliating seurological disease, conclassical cadherin-expressing cells, inhibiting synaptic stability in nonclassical cadherin-expressing cells, inhibiting synaptic stability in conclassical cadherin-expressing calls, inhibiting synaptic stability in conclassical cadherin-expressing calls, inhibiting synaptic stability in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age related macrolar degeneration, multiple solerosis and inbioreactors. AAV66522 to AAX64572 represent specifically claimed peptides, and in AAX6572 represent specifically claimed peptides, and in the contrast of the process the contrast in a mammal in they can also be used for detection and diagnosis and in bioreactors. AAX6652 to AAX64572 represent specifically claimed peptides, and in the contrast in the process the contrast in the process in the contrast in the contras
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention
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Claim 54; Page 184; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.5%;
57.1%;
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Best Local Similarity
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CVPLTSC 7

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AAY62224 standard; peptide; 7 AA.

RESULT 15

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AAY62224;

AAY62224 ID AAY6 XX XX AC AAY6 XX

Search completed: March 8, 2004, 12:29:28 Job time : 53 secs

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March 8, 2004, 12:30:49; Search time 33 Seconds (without alignments) 44.790 Million cell updates/sec
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1: /cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*

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11: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

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15: /cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

16: /cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        809742 seqs, 211153259 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                        US-09-761-636A-11
42
1 CVPLTSC 7
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Maximum DB seq length: 7
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		7	Sequence 8, Appli	Sequence 8, Appli	Sequence 1375, Ap	Sequence 1375, Ap	Sequence 1799, Ap	Sequence 3971, Ap	Sequence 4047, Ap	Sequence 1799, Ap	Sequence 3971, Ap	Sequence 4047, Ap	Sequence 3574, Ap	Sequence 3574, Ap	Sequence 1392, Ap
ΩI	US-09-761-636A-11	US-09-761-636A-12	US-09-932-613-8	US-09-932-322-8	US-10-006-869-1375	US-10-395-032-1375	US-10-006-869-1799	US-10-006-869-3971	US-10-006-869-4047	. US-10-395-032-1799	US-10-395-032-3971	US-10-395-032-4047	US-10-006-869-3574	US-10-395-032-3574	US-10-006-869-1392
DB	6	σ	10	10	14	15	14	14	14	15	15	15	14	15	14
% Query Match Length DB	7	9	7	7	7	7	7	7	,	7	-				
% Query Match	100.0	69.0	66.7	66.7	61.9	61.9	59.5	59.5	59.5	59.5	50	9	57.1	57.1	54.8
Score	42	29	28	28	26	26	25	25	25	25	25	25	24	24.	23
Result No.	-	7	m	4	ľ	ı ve	7	· oc	, σ	0.	= 1	12	1 .	14	15

; Sequence 12, Application US/09761636A; Patent No. US20020065218A1

RESULT 2 US-09-761-636A-12

	Sequence 4041, Ap Sequence 1392, Ap Sequence 1740, Ap Sequence 2155, Ap	2720, 3637, 4041, 35, Ap	225 188 275 360	e 3621, e 1888, e 2750, e 3601,	Sequence 184, App Sequence 186, App Sequence 103, App Sequence 183, App Sequence 187, App Sequence 2748, App Sequence 3576, App
US-10-006-869-1740 US-10-006-869-2155 US-10-006-869-2720 US-10-006-869-3637	US-10-006-869-4041 US-10-395-032-1392 US-10-395-032-1740 US-10-395-032-2155	10-395-032- 10-395-032- 10-395-032- 10-083-894-	10-006- 10-006- 10-006- 10-006-	0-006-869- 0-395-032- 0-395-032- 0-395-032-	US-09-911-838-184 US-09-911-838-186 US-09-765-086-103 US-09-911-838-185 US-09-911-838-185 US-09-911-838-187 US-10-006-869-2748
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ALIGNMENTS

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RESULT 1
US-09-761-636A-11
US-09-761-636A
; Sequence 11, Application US/09761636A
; Patent No. US202065218A1
; Sequence 11, Application US/09761636A
; Patent No. US202065218A1
; Sequence 11, Application US/09761636A
; Patent No. US202065218A1
; Patent No. US202065218A1
; Patent No. US202065218A1
; PRIZAMT: STACKER, Steven
; APPLICANT: STACKER, Steven
; APPLICANT: GARDON, MAGEL
; DIS REPREMENT: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/76,636A
; CURRENT PILING DATE: 2000-01-18
; PRIOR FILING DATE: 2000-01-18
; PRIOR PLING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-01-18
; PRIOR PLING DATE: 2000-01-18
; PRIOR PLING DATE: 2000-01-18
; PRIOR PLING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR PLING DATE: 2000-01-18
; PRIOR PLING DATE: 2000-01-18
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILIN
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APPLICANT: Dyax Corp.
APPLICANT: Beltzer, M. Daniel
APPLICANT: Petter, M. Daniel
APPLICANT: Petter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLyS)
FILE REFERENCE: Dyx-018.1 PCT; DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARR: Patentin version 3.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1375, Application US/1006869
; Sequence 1375, Application US/1006869
; Publication No. US20030082166A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Symonds, James Matthew
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CAMPARIALW-MEDIATED FUNCTIONS
; TITLE OF INVENTION: CAMPARIALW-MEDIATED FUNCTIONS
; FILE REPERENCE: 100086.407C7
; CURRENT PLILIG DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Extentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: BLyS binding polypeptide
NAME/KEY: MISC FEATURE
LOCATION: (2)...(2)
OTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably Tyr);
NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (4)...(4)
; OTHER INFORMATION: X4 is Pro or Tyr (preferably Pro);
US-09-932-322-8
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Sequence 1375, Application US/10395032

Publication No. US20030229199A1

GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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57.1%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.14
4; Conservative
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Best Local Similarity 57.1.
"has 4; Conservative
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US-10-006-869-1375
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LENGTH: 7
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SEQUENCE 8, APPLICATION US.20030091565A1

PUBLICATION NO. US.20030091565A1

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Potter, James P.
APPLICANT: Rosen, Craig A.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REPRENCE: Dyx-025.1 PCT; DYX-025.1 US
CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
ILENGTH: 7
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             GENERAL INFOGUELIAL METCHEN, WATCH APPLICANT: ACHEN, WATCH APPLICANT: STACKER, Steven APPLICANT: STACKER, Steven APPLICANT: GENDROW, Angela APPLICANT: CENDROW, Angela APPLICANT: CENDROW, Angela CURENT CENDROW: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR FILE REFRENCE: 106448656 Achen et al CURRENT PELICATION NUMBER: US/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-05-16 PRIOR FILING DATE: 2000-05-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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LOCATION: (2)...(2)
OTHER INFORMATION: X2 is Phe, Trp, or Tyr (preferably Tyr);
NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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69.0%; Score 29; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 7.2e+05;
Matches 5; Conservative 0; Mismatches 0;
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Publication No. US20030194743A1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 4; Conserv
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   SENERAL INFORMATION:
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US-09-932-322-8
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CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3971
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ORGANISM: Artificial Sequence
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US-10-395-032-1799
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US-10-006-869-4047
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C7
CURRENT APPLICATION NUMBER: US/10/006,869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.40712
CURRENT APPLICATION UNMERR: US/10/066,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1799
          APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
CURRENT APPLICATION NUMBER: US/10/395,032
CURRENT FILING DAIE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO 1375
LENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-7 cell adhesion recognition sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.9%; Score 26; DB 15; Length 7; 57.1%; Pred. No. 7.2e+05; tive 0; Mismatches 3; Indels
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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; Sequence 1799, Application US/10395032;
; Sequence 1799, Application No. US20030229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.; APPLICANT: Symonds, James Matthew
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHENIN-MEDIATED FUNCTIONS
; FILE REPRESENCE: L000086.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1799
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APPLICANT: Blaschuk, Orese W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4047
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                                                                                                                  OTHER INFORMATION: Representative cyclic modulating agent based on corner in Theorem (Control of the Control of the Control of the Control of C
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Pred. No. 7.2e+05;
0; Mismatches 3; Indels
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Publication No. US20030082166A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 57.1%;
Matches 4; Conservative (
TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 57.1.",
--hog 4; Conservative
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US-10-395-032-3574
US-10-395-032-3574
is Sequence 3374, Application US/10395032
publication No. US20030229199A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: CADHERIN-MEDIATED FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPREMENT OR: 100066.40709
CURRENT APPLICATION NUMBER: 105/10/395,032
CURRENT PILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3574
                                                                                                                                                                                  US-10-006-8699-3574

| Sequence 3574, Application US/10006869
| Sequence 3574, Application US/10006869
| Publication No. US20030082166Al
| GENERAL INRORMATION:
| APPLICANT: Blaschuk, Orest W. | APPLICANT: Symonds, James Matthew | APPLICANT: Gour, Barbara J. | ITLL CANT: Blaschuk, CADHERIN-MEDIATED FUNCTIONS | TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS | TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS | TITLE OF INVENTION: 0.0106.407C7 | CURRENT PILING DATE: 2001-12-03 | NUMBER OF SEQ ID NOS: 4052 | SOUTHARE: Patentin Ver. 2.0 | SEQ ID NO 3574 | IENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion corner INFORMATION: recognition sequence US-10-006-869-3574
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Best Local Similarity 42.9%; Pred. No. 7.2e+
Matches 3; Conservative 2; Mismatches
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Best Local Similarity 42.9
Matches 3; Conservative
       4; Conservative
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1 CDPVSGC 7
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; Sequence 4047, Application US/10395032
; Publication No. US20000229199A1
; Publication No. US20000229199A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADRENIA-MEDIATED FUNCTIONS
; TITLE OF INVENTION: CADRENIA-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.497C9
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTHARE: PatentIn Ver. 2.0
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APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADBERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C9
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SEQ ID NOS: 4052
SEQ ID NO 3971
LENGTH: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: cadherin-14 cell adhesion recognition sequence US-10-395-032-3971
                                    CTHER INFORMATION: Representative cyclic modulating agent based on CTHER INFORMATION: cadherin-12 cell adhesion recognition sequence US-10-395-032-1799
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                                                                                                                                        Score 25; DB 15; Length 7; Pred. No. 7.2e+05; Mismatches 3; Indel8
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ORGANISM: Artificial Sequence
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                                                                                                                                                59.5%;
57.1%;
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Best Local Similarity 57.1%
Matches 4; Conservative
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US-10-395-032-3971
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RESULT 15
Use 1922, Application US/10006869
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Best Local Similarity
Matches 5; Conserv
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Sequence 150, App
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                                                                                                      March 8, 2004, 12:08:26; Search time 23 Seconds (without alignments) 24.691 Million cell updates/sec
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1. /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6. /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S-09-601-729-204
S-08-836-075A-187
S-08-331-383-31
S-08-549-008-42
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Match Length DB
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Maximum DB seq length: 11
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Sequence 142, App
Sequence 144, App
Sequence 147, App
Sequence 148, App
Sequence 147, App
Sequence 147, App
Sequence 148, App
Sequence 3, Appli
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Sequence 3, Appli
Sequence 15, Appli
              Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                             Sequence 150, Application US/08189331

Patent No. 574734
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TERE: FLOUPEY ALLOAD
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: CONCURTENTLY herewith
CLASSIFICATION: 435
ATTORNEY/ACBNT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 1101-155
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
TEMPORATION FOR SEQ ID NO: 150:
SEQUENCE CHARACTERISTICS:
TEMPORATION FOR REQ ID NO: 150:
 US-08-802-981-142
US-08-802-981-144
US-08-189-331-148
US-08-189-331-148
US-08-189-331-148
US-08-471-068-149
US-08-471-068-149
US-08-471-068-149
US-08-471-068-148
US-08-467-083-3
US-08-468-348A-3
US-08-466-680B-3
US-08-466-680B-3
US-08-466-680B-3
US-08-466-680B-3
US-08-466-680B-3
US-08-466-5453-3
                                                                                                                                                                                                                                                             US-08-033-857A-5
                                                                                                                                                                                                                                               PCT-US95-01672-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-08-189-331-150
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Gape

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49.2%; Score 30; DB 1; Length 8; 62.5%; Pred. No. 3e+05; tive 1; Mismatches 2; Indels

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Sequence 5, Application US/08900321

Sequence 5, Application US/08900321

Patent No. 5981712

GENERAL INFORMATION:
APPLICANT: Kin, Young S.
TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and TITLE OF INVENTION: 1085 Thereof
ITLE OF INVENTION: 1085 Thereof
INTER OF INVENTION: 1085 Thereof
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CORRATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,190A
FILING DATE: 14-MR-1994
CLASSIFICTATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HUNTEY, TOM
REFREENCE/DOCKET NUMBER: 38,498
REFREENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARRACTERISTICS:
LENGTH: 10 amino acids
MEDIUM STATESTICE:
MEDIUM STATESTICS:
MEDIUM ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.3%; Score 27; DB 1; Length 10; 62.5%; Pred. No. 1.6e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTRY: California
CONTRY: USA
ZIP: 9411-1334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,321
FILING DATE: 14-MA-194
ATTORNEY/ACRTIN NUMBER: US 08/212,190
FILING DATE: 14-MA-194
ATTORNEY/ACRTIN NUMBER: 38,498
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 38,498
REGISTRATION NUMBER: 18,76-0200
TELEPRAX: (415) 576-0200
TELEPRAX: (415) 576-0200
TELEPRAX: (415) 576-0200
TELEPRAX: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5'
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: peptide US-08-212-190A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VPPAPVPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-08-900-321-5
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APPLICANT: KOHN, Elise C.
APPLICANT: LIOTTA, Lance A.
APPLICANT: LIOTTA, SON
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: Stan Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                  Sequence 150, Application US/08471068

Factor No. 5948635

Factor No. 5948647

FAPLICANT: Kay, B. K.

APPLICANT: Fowlkes, D. M.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 186

CORRESONDENCE ADDRESS:

CORRESONDENCE Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.2%; Score 30; DB 2; Length 8; 62.5%; Pred. No. 3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
INEW TOOS-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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US-08-212-190A-5
; Sequence 5, Application US/08212190A
; Patent No. 5652223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECHONN: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 6644 PENNIE
INFORMATION FOR SEQ. ID NO: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 maino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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MOLECULE TYPE: peptide

US-08-471-068-150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105-1493
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                                                                                    RESULT 2
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; Patent No. 574734
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
APPLICANT: Kay, B. K.
APLICANT: Rowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
COMESSONDENE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
CONNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.6%; Score 26; DB 1; Length 8; 57.1%; Pred. No. 3e+05; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                      42.6%; Score 26; DB 2; Length 6; 83.3%; Pred. No. 3e+05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN ROLENE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: CONCULTENTLY herewith
FILE REFERENCE: BRU96-02
CURRENT APPLICATION NUMBER: US/08/769,745
CURRENT FILING DATE: 1996-12-19
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 15
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Miscrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEFRA: 212 869-8864/9741
TELEFRA: 66141 FENNIE
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CISVPLT 7
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                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                               5 PLTSVP 10
                                                                                                                                                                                                                                                                                                                                                      PLTPVP 6
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
US-08-189-331-149
                                                                                                                                               ; TYPE: PRT
; ORGANISM: Rat
US-08-769-745-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
USBS THEREOF
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03610
FILING DATE: 14-MAR-1995
CLASSIFICATION NUMBER: US 08/212,190
FILING DATE: 14-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.3%; Score 27; DB 5; Length 10; 62.5%; Pred. No. 1.6e+02; tive 0; Mismatches 3; Indels
                                                                                                                                                                  Query Match
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08769745
Patent No. 595529
GENERAL INFORMATION:
APPLICANT: Holmes, Todd C.
APPLICANT: Levitan, Irwin B.
APPLICANT: Sanddei University
APPLICANT: BOT INVENTION: Mechanism for the Regulation of Ion; TITLE OF INVENTION: Channel Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 15280-204000PC
REFERENCE/DOCKET NUMBER: DHUS Ref. No. E-112-94/0
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                             RESULT 5
PCT-USOS-03610-5
; Sequence 5, Application PC/TUS9503610
; GENERAL INFORMATION:
                       : LENGTH: 10 amino acids

: TYPE: amino acid

: STRANDENESS:

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

US-08-900-321-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.3
Best Local Similarity 62.5
Matches 5; Conservative
        SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear _ MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VPLTSVPC 11
                                                                                                                                                                                                                                                         4 VPLTSVPC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                              1 VPPAPVPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08-769-745-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US95-03610-5
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Gaps

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION WOMBER: US/08/331,383
FILING DATE: 28-OCT-1994
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/331,383
APPLICATION NUMBER: US 08/331,383
APPLICATION NUMBER: US 08/331,383
APPLICATION NUMBER: US 08/331,383
RESISTENCE, DIED LAUVER
RESISTENCE/DOCKET NUMBER: 016865-000110US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               NAME: DOW, KATEN B.
REGISTRATION NUMBER: 29,684
REPERENCE/DOCKET NUMBER: 16865-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Application US/08549008
Patent No. 5714342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide US-08-331-383-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SVPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AIPM-SIPC 9
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US-08-549-008-43
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Sequence 33, Application US/08331383
Patent No. 5605809
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Romoriya, Akira
APPLICANT: Compositions for the Detection of
TITLE OF INVENTION: Proteases in Biological Samples and Methods and Use
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
GORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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              Sequence 149, Application US/08471068
Patent No. 5948635
GENERAL INFORMATION:
APPLICANT: KAY, B. K.
APPLICANT: FOWIKES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
42.6%; Score 26; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                           ADDRESSEE: Remaie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: US.A.
ZIP: 10036-2711
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1101-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Migrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPRONE: 212 780-9090
TELEFAX: 212 86-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: One max...
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CISVPLT 7
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US-08-331-383-33
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GENERAL INFORMATION:
APLICANT: Komoriya, Akira
APLICANT: Komoriya, Akira
APLICANT: Komoriya, Akira
APLICANT: Cardard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Compositions for the Detection of
TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STREET: Two Embarcadero Center, Bighth Floor
COUNTRY: USA
ZIP 94411-3834
COUNTRY: USA
ZIP 94411-3834
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
COMPUTER: LEM PC compatible
COMPUTER: LEM PC compatible
COMPUTER: LEM PC compatible
COMPUTER: USA
COMPUTER: Tab PC compatible
COMPUTER: USA
COMPUTER: US
                                                                                                                                                                ü
                                                                                                                                                                Gaps
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Query Match
41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels
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Sequence 26, Application US/08483077C

Patent No. 5813391

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tempczyk, Anna
APPLICANT: Tempczyk, Anna
APPLICANT: Thengus, Martano J.
APPLICANT: Zheng, Zhong-Li

TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBERS OF SEQUENCES: 33
CORRESONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Phakellistatin 10

NAME/KEY: amino acid analysis, high resolution

NAME/KEY: motlear magnetic resonance and mass

NAME/KEY: spectral MS/MS techniques

OTHER INFORMATION: Phakellistatin 10 is a

OTHER INFORMATION: cell growth inhibitory peptide with

OTHER INFORMATION: cell growth inhibitory peptide with

OTHER INFORMATION: cell line of 2.1 mg/ml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 1; Length B;
Pred. No. 3e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                      ZIP: 85258-1234
COMPUTER REARABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS 5
                                                                                                                                                                                                                                                             CURRATING SYSTEM: DOS 5
SOFTWARE: Microsoft Word for Windows CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,239B
FILING DATE: 12/20/94
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD WINBER: 17,886
REGISTRATION NUMBER: 17,886
REGISTRATION NUMBER: 4997
TELEPHONE: (602)-483-1285
ITELEPHONE: (602)-483-1285
INFORMATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
TYPE: amino acid
TYPE: AMINO ACID
DESCRIPTION: Cyclic
MOLECULE TYPE:
DESCRIPTION: Cyclic
DESCRIPTION: Cyclic
DESCRIPTION: Cyclic
DESCRIPTION: DARKellistatin 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: circular
ORIGINAL SOURCE:
ORGANISM: Phakellia sp.
DEVELOPMENTAL STAGE: whole organism
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Richard R. Wybeck
STREET: 8010 East Morgan Trail, #10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%;
66.7%;
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Best Local Similarity
Matches 4; Conserv
                                                                                                    Scottsdale
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                                                                                                                                 Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-483-077C-26
                                                                                               CITY: Scc
STATE: A:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-360-239B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Komoriya, Akira
APPLICANT: Romoriya, Akira
APPLICANT: Packard, Beverly S.
TITLB OF INVENTION: Compositions for the Detection of Enzyme
TITLB OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                 Gaps
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the Human Cancer Cell Growth Inhibitory Cyclic
Octapeptides Phakellistatin 10 and 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                            Query Match
41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: F10PDPy disk
COMPUTER. THEN PC COMPATIBLE
COMPUTER: F10PDPy disk
COMPUTER: F10PDPy disk
COMPUTER: F10PDPy disk
COMPUTER: P40PDPy disk
SOFTWARE: P40PDPY disk
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION 10PCRATION:
NAME: HUNTER, TOM
REGISTRATION NUMBER: 38 4.98
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08360239B Patent No. 5801222 GENERAL INFORMATION: APPLICANT: Pettit, George R. APPLICANT: Tan, Rui TITLE OF INVENTION: Isolation and S TITLE OF INVENTION: Octapoptides Ph ITLE OF INVENTION: Octapoptides Ph
                                                                                                                                                                                                                                                                                                                                                       Sequence 143, Application US/08802981; Patent No. 6037137
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SVPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AIPM-SIPC 9
                                                                                                                                                                                      3 SVPLTSVPC 11
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2 AIPM-SIPC 9
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Matches 4; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-802-981-143
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US-08-360-239B-1
                     US-08-549-008-43
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0; Gaps
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GENERAL INFORMATION:

APPLICANT: TSeng-Law, Janet
APPLICANT: Guillermo, Roy
APPLICANT: Guillermo, Roy
APPLICANT: Helgerson, Sam L.
APPLICANT: Helgerson, Sam L.
APPLICANT: Helgerson, Robert J.
TITLE OF INVENTION: Deans, Robert J.
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Invine
STREET: P.O. Box 15210
CITY: Invine
STREET: P.O. Box 15210
COMPUTER: California
COUNTRY: USA
ZIE: 9213-5210
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BAFICATION ADTA:
APPLICATION WHERE PAGENES
SOFTWARE: PATCHIN DATA:
APPLICATION WHERE Janice
CLASSIFICATION WHERE: 1744 440-5353
TELECOMMUNICATION INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 1744 440-5353
TELECOMMUNICATION NUMBER: 174 440-5353
TELERAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH I D amino acide
TUTNO TOR SEE DEAD ACIDE
TELENGES AND ACIDE
TELENGES CHARACTERISTICS:
LENGTH I D amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.0%; Score 25; DB 2; Length 10; Best Local Similarity 66.7%; Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                             LOCATION: 10 | OTHER INFORMATION: /note= "The carboxy-terminus is a OTHER INFORMATION: carboxamide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
41.0%; Score 25; DB 2; I
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3;
REFERENCE/DOCKET NUMBER: P-CY 1795
TELECOMMUNICATION INFORMATION:
TELEPAX: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 108, Application US/08482228
; Patent No. 596873
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: circular
MOLECULE TYPE: peptide
                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 ISVPLTSVP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LDVPILDVP 10
                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide LOCATION: 10
                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-482-228-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-482-228-108
                                                                                                                                                                                                                                                                                                                                                                                                                                  ÚS-08-519-109B-26
                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
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US-08-519-109B-26
Sequence 26, Application US/08519109B
Sequence 26, Applications Archaelus, Thomas S.
APPLICANT: Tangozyk, Anna
APPLICANT: Tangozyk, Anna
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEB: Campbell & Flores LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.4%; Pred. No. 3.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "The carboxy-terminus is a OTHER INFORMATION: carboxamide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: STATE COMPATIBLE
COMPARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,109B
FILING DATE: 25-AUG-1995
CLASSIFICATION: 514
ATTORNEY AGRENT INCOMMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHION DATA:
APPLICATION NATE: VS/08/483,077C
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 314
ATTORNEY/ACENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 91,815
REFERENCE/DOCKET NUMBER: 31,815
REGISTRATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 10, annino acids
TYPE: annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: San Diego
STATE: California
COUNTRY: United States
                                                          California
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LDVPILDVP 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide LOCATION: 10
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                                                                                    COUNTRY:
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0; Gaps 3; Indels 0; Mismatches 6; Conservative Matches

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Search completed: March 8, 2004, 12:11:49 Job time : 23 sec8

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March 8, 2004, 12:15:17; Search time 13 Seconds (without alignments) 66.594 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                             790
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        283366 seqs, 96191526 residues
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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50
1 CSVPLTSVC 9
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

ss Description	205K exoantigen -	118K stomach cance	Ig heavy chain CRD	glycogen phosphory	MHC H2-L antigen -	T-cell receptor be	T-cell receptor al	major protein anti	T-cell receptor ga	fibroblast growth	neutral proteinase	sperm-activating p	orf dowstream to b	seminal vesicle pr	laminin B1 - weste	Na+/K+-exchanging	formylglycinamide	aggrecan - bovine	metallothionein is	unidentified 6.5/3	•н	hypothetical colla	seed protein ws-5	alcohol dehydrogen	enamelin f - bovin	coat protein beta	kidney and bladder	endosperm protein,	tvrosine-melanocvt
SUMMARIES	G33098	A60356	PT0247	A60521	165546	PH0932	PH0803	E60274	F41946	A42057	A35180	A60522	B41983	I52974	I49421	S29881	A12016	S42620	S59622	PQ0701	PT0268	A35039	E61491	871919	\$10783	S13636	G58502	S70334	A32039
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Score	17	16	16	15	15	15	15	14	14	14	14	14	14	14	13	13	13	13	13	13	13	12	12	12	12	12	12	12	-
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RESULT 3
PT0247
Ligheavy chain CRD3 region (clone 2-106A) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

schwannomin - mous R-phycoerythrin al	dnaA protein - Pse Ig heavy chain CRD	catch-relaxing pep dihydrofolate redu	DNA topoisomerase	Ig H chain V-D-J r acylase - Kluyvera	endoglycosylcerami	nitrate reductase lectin - potato (f	T-cell receptor be	gene Cftr protein	major postsynaptic	granulocyte-colony
I54357 B22565	B34835 PT0280	ECMUCR 148105	148086	PH1602 S19288	B39745	S21288	PT0530	157018	A42689	154017
4.0	9 9		7	7 8 7	89	80 80	8	8	8	8
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30	3.62	3.4	36	37 38	39	4 41 11	42	43	44	45

ALIGNMENTS

RESULT 1 G33098 205K exoantigen - malaria parasite (Plasmodium falciparum) (fragments) 205K exoantigen - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C;C;Species: Plasmodium falciparum C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000 C;Accession: G33098 A;Nacelosio, JJH; Hager, L.P. Bubmitted to the Protein Sequence Database, May 1990 A;Reference number: A33098 A;Accession: G33098 A;Accession: G33098 A;Accession: G33098 A;Accession: G33098 A;Accession: G3008 A;Residues: protein	y Match 34.0%; Score 17; DB 2; Length 8; Local Similarity 66.7%; Pred. No. 2.8e+05; Less 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	3 VPLTSV 8 2 VPLXLV 7	RESULT 2 A60356 LI18K stonach cancer antigen - human (fragment) C;Species: Homo sapiens (man) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999 C;Accession: A60356 R;Shiraishi, Y.	Int. J. Cancer 45, 783-787, 1990 A,Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens A,Reference number: A60356; MUID:90216080; PMID:2323853 A,Accession: A6036; MUID:90216080; PMID:2323853 A,Rolecule type: protein A,Residues: 19 <shi> C,Keywords: glycoprotein</shi>	Query Match 32.0%; Score 16; DB 2; Length 9; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0; Matches 3 VPLTSV 8 3 VPLTSV 8 1	
RESULT 1 G33098 205K excentigen C; Species: Plasen C; Date: 24-Aug-19 C; Accession: G330 K; Nichols, U.H.; submitted to the A; Reference numbe A; Accession: G33 A; Accession: G33 A; Accession: G33 A; Accession: A; Residues: 1-8	Query Match Best Local S Matches 4	Qy 3	RESULT 2 A60356 118K stomach can C;Species: Homo C;Date: 12-Feb-C;Accession: A6	Int. J. Cancer 45, A;Title: Western b A;Reference number A;Accession: A6035 A;Molecule type: p A;Residues: 1-9 <s c;keywords:="" glycop<="" td=""><td>Query Match Best Local s Matches 3 Oy 3</td><td>97</td></s>	Query Match Best Local s Matches 3 Oy 3	97

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C. Species: Wycobacterium tuberculosis
C. Species: Wycobacterium tuberculosis
C. Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C. Accession: 860274
R. Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R. Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R. Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
A. Title: Isolation and partial characterization of major protein antigens in the culture and the second second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T.C. In receptor alpha chain (J2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PHO803
R;Casanova, J.L; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
J. Ayritle: T cell receptor appending a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire.
A;Reference number: PHO746; MUID:92078846; PMID:1836010
T.coll receptor beta chain V-D-J region (clone 3) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: PH0932
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1475, 1991
J. Hitle: Analysis of T cell receptor beta chains in Lewis rats with experimental aller:
A;Reference number: PH0891; MUID:92078857; PMID:1836012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                  A;Accession: PH0932
A;Wolecule type: mRNA
A;Residues: 1-7 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 15; DB 2; Length 8;
Pred. No. 2.8e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15; DB 2; Length 7; Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor
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33.3%;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity 33.3
Matches 2; Conservative
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Best Local Similarity 50.03
Matches 2; Conservative
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A;Molecule type: protein
A;Residues: 1-5 <NAG>
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1 CAAGIT 6
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A, Molecule type: mRNA
A, Residues: 1-8 < CAS>
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C;Species: Wus musculus (house mouse)
C;Species: Wus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 165546
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.
A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and theil A;Reference number: 152778; MUD:86106202; PMID:3510743
A;Accession: 165546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Reynords: glucan phosphorylase
C;Reynords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 17-Apr.1993 #sequence_revision 17.Apr.1993 #text_change 18-Aug-2003
C;Accession: A60521
R;Bonamusa, L; Baanante, I.V.
R;Bonamusa, L; Baanante, I.V.
A;Title: Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
                  R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A;File: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Accession: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0347
A;Molecule type: DNA
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N,Alternate names: glycogen phosphorylase b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.8e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                        Query Match
32.0%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                A Experimental source: B lymphocyte C; Keywords: heterotetramer; immunoglobulin
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75.0%;
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SAPIDS 7
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   C; Accession: PT0247
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3 PIT 5

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RESULT 6

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Grant activating peptide SAP-IV - sea urchin (Diadema setosum)
C;Species: Diadema setosum
C;Species: Diadema setosum
C;Species: Diadema setosum
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60522
R;Yoblino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suz_romp, Biochem. Physiol. B 95, 423-429, 1990
A;Title: A species-specific sperm-activating peptide from the egg jelly of the sea urc A;Reference number: A60522; MUID:90227916; PMID:2158412
A;Molecule type: protein
A;Molecule animal peptides
F;2-9/Disulfide bonds: #status experimental
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R,Teng. C.T.; Harris, S.E.
DNA 2, 105-111, 1981
A;Ttle: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sit A;Reference number: IS2974; MUID:83261204; PMID:6307619
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C;Species: Azotobacter vinelandii
C;Species: Azotobacter vinelandii
C;Date: ol-War-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: B41983
R;Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, B.I. Proc. Natl. Acad. Sci. U.S.A. 89; 2419-2423, 1992
A;Title: Unification of the ferritin family of proteins.
A;Reference number: A41983; MUID:92196129; PMID:1549605
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
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A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid; protein
A;Residues 1.9 GGRO-
A;Cross-references: GB:M03692; NID:g142297; PIDN:AAA22122.1; PID:g142299
A;Note: sequence extracted from NCBI backbone (NCBIP:09442)
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A;Gene: SVSIV
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C;Species: Mus musculus (house mouse)
C;Date: (03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: F41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
Mylitle: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A;Reference number: A41946; MUID:92049316; PMID:1658619
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Diol. Chem. 265, 5809-5815, 1990
A.fitle: Purification of a novel type of calcium-activated neutral protease from rat bra
A.Reference number: A35180; MUID:90202830; PMID:2318836
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A/Title: Differential splicing in the extracellular region of fibroblast growth factor A;Reference number: A42057; WUID:92107200; PMID:1309595
A;Accession: A42057
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C;Accession: A42057
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C;Accession: A35180
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                                                                                                                    I-cell receptor gamma chain (1a.27) - mouse (fragment)
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A;Residues: 1-8 AVRRA
A;Cross-references: GB:M80363
C;Keywords: growth factor receptor
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A;Residues: 1-8 <YOS>
C;Keywords: hydrolase
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Query Match

Dest Local Similarity 75.0%; Pred. No. 2.8e+05;

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SITSL 6

RESULT 15

149421

13 INSL 6

RESULT 15

149421

149421

149421

149421

15.0% western wild mouse (fragment)

C.Species: Mus spretus (western wild mouse)

C.Species: Jay-135.7, 1994

Max.cession: 149421

A.Filtle: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A.Filtle: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

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~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~		STANDARD;	24, C 24, L 34, L Otein methy		. PubMed=2308822 J., Karran P.; no acid sequence	"; 18:1' hir of the all	inactivated. TIVITY: DNA (cysteine = DN Ysteine. WITH SEGMENTS	H ENCOMPASS THE ALKYL-ACCEI); IPR001497; Methyltransf_1; PS00374; MGMT; PARTIAL. it; Transferase; Methyltran	967 M	38 28 vativ	6 6	STANDARD;	34, C 34, L
000000000000		STP	P 1	vine azod eria ae;	12; 11;	Reparation of the	17. 18. 19. 19. 19. 19.	MPA. 0149 74; ansi	100 kg	11 (1)		ST	(Rel. (Rel. (Rel.
100000000000000000000000000000000000000		í	DNA R. R.	(Bovine). Metazoa; Eutheria; Sovinae; Bo	749; 749; Ha.	fer ds J N: J rrij	1 - L - L - L - L - L - L - L - L - L -	ENCOMPASS IPR001497; SS00374; MC	16 6 6 6 7 6		VPLTSVC : PILTPC		
		T 1 BOVIN MGMT BOVIN P29177;	01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence 01-OCT-1996 (Rel. 34, Last amotatic Methylated-DNAprotein-cysteine met	r. taurus aryota; malia; E idae; Bc I_TaxID=	Li SEQUENCE. TISSUE=Thymus; MEDLINE=90174912; Pu Rydberg B., Hall J., "Active site amino a.	methyltransferase.", Nucleic Acids Res. 18:17-21(1990)!- FUNCTION: Repair of alkylated transferring the alkyl group a residue in the enzyme. This is	<pre>irreversibly inactivated. :!- CATALYTIC ACTIVITY: DNA ([protein]-L-cysteine = DN S-methyl-L-cysteine. :!- SIMILARITY: WITH SEGMENTS</pre>	WHIC SITE; repe		Query Match Best Local Simi] Matches 2; (3 VP	r 2 arma act carma sentos.	01-0CT-1996 01-0CT-1996 15-JUL-1999
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TISSUE-Skin secretion;
Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
"Peptides from the skin glands of the Australian buzzing tree frog
Litori electrica. Comparison with the skin peptides from Litoria
rubella.";
                                                                                                                                                                                                                                                                                                                                  Liforia rubella (Desert tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duve H., Johnsen A.H., Maeetro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
-I. SIMILARITY: Belongs to the allatostatin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cydia pomonella (Codling moth).
Bukaryota, Metazoa, Arthropoda; Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia;
Tortricoidea, Tortricidae, Olethreutinae, Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.0%; Score 13; DB 1; Length 6; 66.7%; Pred. No. 1.4e+05; tive 1; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 24.0%; Score 12; DB 1; Length 8; Best Local Similarity 66.7%; Pred. No. 1.4e+05; Matches 2; Conservative 1; Mismatches 0; Indels
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA; 936 MW; 0B2879C45B573767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
    75.0%; Pred. No. 1.4e+05; iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 6.
                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                             6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aust, J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=98054539; PubMed=9392829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 66.7
nes 2; Conservative
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MOD_RES 8 8
                            Conservative
                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               Pelodryadinae, Litoria.
NCBI TaxID=104895;
Best Local Similarity
Matches 3; Conserv
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                                                                   4 PLTS 7
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2 VPI 4
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P82157;
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                                                                                                                                                                                                                                                                                                in all eukaryotic cells.
--- SUBCELLANE LOCATION: Cytoplasmic.
--- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
6.8, ITS MM IS: 46 kDa.
--- SIMILARITY: Belongs to the actin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                    FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed
                                                                                                                                                                                                             "A transaldolase. An enzyme implicated in crab steroidogenesis."; Endocrine 5:23-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
o
                                                                                                                                                                         Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actin (Fragment).

Carcinus maenas (Common shore crab) (Green crab).

Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.

NCBL_TaxID=6759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 14; DB 1; Length B;
Pred. No. 1.4e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stiefel B.I.;
"Unification of the ferritin family of proteins.";
Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 9 AA; 947 MW; DF98B5A1B417776D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA; 976 MW; 1424005AB2CAAEB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
16-CCT-2010 (Rel. 40, Last amoutation update)
Hypothetical protein in bfr 3'region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AY.
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004001; Actin.
InterPro; IPR004001; Actin. Like.
PROSITE: PS00406; ACTINS_I; PARTIAL.
PROSITE; PS00412; ACTINS_2; PARTIAL.
PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.0%; Score 14;
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40.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; B41983; B41983.
Hypothetical protein.
NON TER 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                Baghdassarian D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CDVDI 6
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P25825 YBFR AZOVI

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TISSUE-EPpetralk;
MEDLINE-21956277; PubMed=11959015;
MEDLINE-21956277; PubMed=11959015;
MIDLINE-21956277; PubMed=11959015;
MIDLINE-21956277; PubMed J., Krungskasen C., Longyant S.,
Charvisuthangkura P., Sithigorngul W., Petsom A.,
"Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
Comp. Biochem. Physiol. 118:355-337 (2002).
-- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treponema hyodysenteriae (Serpulina hyodysenteriae).
Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
NCBL_TaxID=159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
PERREmide-like neuropeptide FLP5 (SMPSLRIRF-amide).
Penaeus monodon (Penoeid shrimp).
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
NCBI_TAXID=6687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.
-!- SIMILARITY: Belongs to the PARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0007218; P:neuropeptide signaling pathway; TAS. Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 9 AMIDATION.
9 AA; 1106 MW; B60B07340735A766 CRC64;
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-1- SUBCELLULAR LOCATION: Periplasmic flagellum.
                                                                                     9 AA.
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66.7%;
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                                                                                   STANDARD;
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UNSURE 2 2
UNSURE 8 9
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les 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
FLAA2.
                                                                                   PENMO
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SEQUENCE
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Best Local S
                                   RESULT 8
FARS PENMO
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Electrophoresis 13:707-714(1992).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 4.9, its MW is: 65 kDa.
SWISS-2DPAGE; P30087; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                               15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Allergen Rus 13596* (Fragment).
Fusarium solani (subsp. pisi) (Nectria haematococca).
Hyporromy, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hyporromycetiade; Hyporreales; Nectriaceae; Nectria.
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01-APR-1993 (Rel. 25, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUB=Plasma;
MEDLINE=93022937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Hughes G.J.C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 12; DB 1; Length 8; Pred. No. 1.4e+05; 1; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=TARI 3596; TISSUE=Mycelium;
Verma J., Gangal S.V.;
Submitted (JUL-1997) to Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 8 AA; 898 MW; C372C441F5B69041 CRC64;
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                                                                                                                                                                              8 AA.
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3 VPL 5
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1 LPL 3
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6 NVP 8
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5 NVP 7
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UPA1_HUMAN
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Bufo regularis (Leopard toad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Bufonidae, Bufo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=5605313; PubMed=7591488; Chau J., Chait B.T., Acher R.; Chauvet J., Michel G., Ouedraego Y., Chou J., Chait B.T., Acher R.; A new neurohypophysial peptide, seritocin ([Ser5,Ile8]-oxytocin), identified in a dryness-resistant African toad, Bufo regularis."; Int. J. Pept. Protein Res. 45:482-487(1995).

-! FUNCTION: Devoid of oxytocic activity.

-! SUBCELLULAR LOCATION: Secreted.

-! SIMILARITY: Belongs to the vasopressin/oxytocin family. InterPro: IPR002981; Neurhyp_horm.
Pfam; PF00220; hormone4; 1.

PROSITE: PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elssmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
NCBL_TaxID=7797;
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isolated from the spotted dogfish (Scyliorhinus caniculus).", Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
-i- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
-i- SINILARITY: Belongs to the vacopressin/oxytocin family. InterPro; IPR000981; Neurhyp_horm.
Pfam: PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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Pred. No. 1.4e+05;
0; Mismatches 1; Indels
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17EDD76EB44449DB CRC64;
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9 AA; 983 MW; 17FF476EA5A6D04B CRC64;
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50.0%; Pred. No. 1.4e+05;
tive 1; Mismatches 1;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Valitocin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Seritocin ([Ser5,11e8]-oxytocin).
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nes 2; Conservative
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P43000;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinides; Scyliorhinus.
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MEDLINE=95062247; PubMed=7972045;
Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
"Special evolution of neurchypophysial hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytocin-like peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-SOCIATY, PubMed=7972045;
Chauvet M.-T., Acher R.;
Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
Chauvet J., Rouille Y., Chauveau C.,
Chauvet J., Rouille Y., Chauveau C.,
Chauvet J., Rouille Y., Chauveau C.,
Foulle M., Chaupende J.,
Foulle J., Chaupende J., Wolle J.,
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Pred. No. 1.4e+05;
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                           855A19C68B4772D1 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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2 TVP 4
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01-NOV-1995
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OXYF_SCYCA
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MEDIINE=91101287; PubMed=1846198;
Flanagan W.M., Paparassiliou A.G., Rice M., Hecht L.B.,
Silverstein S., Wagner E.K.;
"Analysis of the herpes simplex virus type 1 promoter controlling the expression of UL38, a true late gene involved in capsid assembly.";
J. Virol. 65:769-786(1991).
--- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
                                                                                                                                                                                                                               MEDLINE=12128038; PubMed=4622083; Acher R., Chauvet J., Chauvet M.-T., Fontaine M.; Valle-oxytocin) and aspartocin (4814-oxytocin) in a selachian fish, the spiny dog-fish (squalus acanthias)."; C. R. Acad. Sci., D. Sci. Nat. 274:313-316 (1972).
1- SIMILARITY: Belongs to the vasopressin/oxytocin family. InterPro; IRR000981; Neurhyp_horm.
PFOSIZE: PS00220; hormone4; 1.
                                          MEDILINE-73031727; PubMed=5083097;
Acher R., Chauvet J., Chauvet M.-T.;
"Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartiladinous fish, Squalus acanthias.";
Eur. J. Blochem. 29:12-19(1972).
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01-NOV-1991 (Rel. 20, Last sequence update)
15-NAR-2004 (Rel. 43, Last annotation update)
Capsid assembly and DNA maturation protein (Virion protein UL38)
(Capsid protein VP19C) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herpes simplex virus (type 1 / strain KOS).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 9 AMIDATION.
9 AA; 996 MW; 17EDD76EB456D04B CRC64;
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les 2; Conservative
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DISULFID 1
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VP19 HSV1K
AC
DC P232I0;
DT 01-NOV-1991
DT 01-NOV-1991
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22.0%; Score 11; DB 1; Length 6;

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                     Gaps
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Brain Res. 422:374-376(1987).
-!- FNOTION: This peptide exhibits both potentiating (contraction) and inhibitory (relaxation) effects on the anterior byssus retractor muscle.
                                                                                                                                                                                                                                                                              MEDLINE=88052022; PubMed=3676797;
Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
Muneoka Y.;
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                     0; Indels
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100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
                                                                                                                                                                                         7 AA.
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                     Conservative
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Matches 1; Congery
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1 AMPM 4
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                                                       4 PL 5
                                                                                        5 PL 6
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Q15890 homo sapien Q15898 homo sapien Q11639 homo sapien Q944m6 staphylococ Q15999 homo sapien Q95/f4 mus musculu Q99/f4 mus musculu Q90/f5 hepatitis b Q90/f0 hepatitis b Q64/72 avian rous-Q64/72 avian rous-P93/80 gallus gall P93/23 lycopersico Q90553 arabidopsis Q45615 bacillus su Q35/60 escherichia Q93/81 prochloroco

07x4q5 nodularia s Q8iv87 homo sapien 002032 lytechinus

P83152 anabaena sp

Q07624 rous sarcom Q9ps68 gallus gall Q67113 influenzavi influenzavi

OM protein

Run on:

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SEQUENCE FROM N.A.
STRAIN=BM3; PLASMID=pKLH207;
KTholdili G.Y., Mindlin S.Z., Gorlenko Z.M., Yurieva O.V.,
Nindlin S.Z., Gorlenko Z.M., Yurieva O.V.,
Petrova M.A., Nikiforov V.G.;
"A young family of transposable adaptive DNA segments identified in
the Acinerobacter genus.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250234; CACGN341; -...
EMBL; AJ486856; CAD31078.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "pKLH2-like aberrant transposons and possible mechanisms of their dissemination.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
NCBL_TaxID=106395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BW3; PLASMID-EXCH207;
Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
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Q3146

Q3146

Q1599

Q1599

Q1599

Q9100

Q91106

Q64972

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Q65184

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Q67113
Q15890
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Q9SAY7
Q9TKF2
Q9TKG1
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Plasmid pKLH207.
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                                                     01-MAR-2003 (
01-MAR-2003 (
01-JUN-2003 (
 Q8GMM5 ;
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08jj20 gallus gall
042564 fugu rubrip
08552 moloney mur
08cgl3 mus musculu
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Q849p4 salmonella
Q9y4x6 homo sapien
Q16468 homo sapien
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                                                                                                          (without alignments)
82.309 Million cell updates/sec
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                                                                                             March 8, 2004, 12:14:57; Search time 34.5 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
                                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
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                                                                    protein search, using sw model
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Q8JJ20
Q8J564
Q85562
Q8CG13
Q8KPX4
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Q9Y4X6
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Q16468
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_invertebrate:*
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Match Length
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Score 20; DB 2; Length 8; Pred. No. 1e+06;

40.0%;

Query Match Best Local Similarity

1 1 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Plasmid. NON TER SEQUENCE

Q81802 zea mays (m Q9tru7 bos taurus 035953 mus musculu Q56140 streptococc Q9tke5 leptospermu Q9md43 rattus norv

035953 Q56140 Q9TKE5 Q9MD43

88511

Result δ.

Matches

ð 임 Q9FXL0 O9FXL0;

RESULT 2

Q9FXL0

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SEQUENCE FROM N.A.

MEDILINE-9742476; PubMed-9295353;
Plummer N.W., Medaler M.H.;
Plummer N.W., McBurney M.W., Medisler M.H.;
Plummer N.W., McBurney M.W., Medisler M.H.;
"Alternative splicing of the sodium channel SCN8A predicts a truncated tro-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:14009-24015(1997).

EMBL, 197673; AAB80916.1;
BMBL, 107673; AAB80916.1;
Oly, CO:0005216; F:ion channel activity; IEA.

NON_TER
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Donoghue D.J., Hunter T.;
"A generalized method of subcloning DNA fragments by restriction site reconstruction. Application to sequencing the amino-terminal region of the transforming gene of Gazdar murine sarcoma virus.";
Nucleic Acids Res. 10:2549-2564(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A.
MEDLINE-83164305; PubMed=6300424;
MEDLINE-83164305; PubMed=5300424;
Donoghue D.J., Hunter T.;
"Recombination junctions of variants of Moloney murine sarcom virus:
Generation and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).
EMBL; K03105; AAA4649.1; -.
ARC2D5BEB44DC76D CRC64;
                                                                                                                                                                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygli; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                                                                                      ol-UAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
SCNBA.
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Pred. No. 1e+06;
0; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2003 (TrEMBLrel. 24, Last annotation update)
01-UN-Cated env protein (Fragment)
Moloney murine leukemia virus.
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SEQUENCE OF 4-8 FROM N.A.
MEDLINE-82196891; PubMed=6281735;
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71.4%;
                                                                       01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2003 (TrEMBLrel. 24,
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Best Local Similarity
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Uefuji H., Takase H., Hiratsuka K.;
Uefuji H., Takase H., Hiratsuka K.;
"Lilium longiflorum LiM8 gene, promoter region and partial sequence.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB050987; BAB1856.1; -.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                 Lilium longiflorum (Trumpet 111y).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Liliales; Liliaceae; Lilium.
VCBI_TaxID=4690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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WARD Q., Li N., Li H.;

Wang Q., Li N., Li H.;

Wang Q., Li N., Li H.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

BMBL; AF487519; AAL96665.1; -.

NON TER

SEQUENCE 7 AA, 780 MW; 72CBIAB2DSBEBB70 CRC64;
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Pred. No. 1e+06;
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Indels
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Extracellular fatty acid binding protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                      Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 9 AA; 1021 MW; 6F8BD76685A6C2CB CRC64;
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                                                                                                                                                                                                                                                                                                                               Last sequence update)
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Mismatches
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(TrEMBLrel. 16, L
(TrEMBLrel. 16, L
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60.0%;
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Best Local Similarity 100.0%,
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4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  IM8 protein (Fragment)
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Q8CG13

RESULT 6 Q8CG13

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SQUENCE FROM N.A.

SQUENCE FROM N.A.

MEDLINE=20108806; PubMed=10640831;
Drechaler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S., Schroth A., Bodem J., Royer-Pokora B.;
Schroth A., Bodem J., Royer-Pokora B.;
"Genomic structure, alternative transcripts and chromosome location of the human LiM domain binding protein gene LDB1.";
Cytogenet. Cell Genet. 87:119-124(1999).

EMBL; AJ243097; CAB45408.1;
NON TER 8
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=9813031;
Markham P.F., Amavisit P., Lightfoot D., Browning G.F.;
"Variation between pathogenic serovars within Salmonella pathogenicity
islands.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1e+06;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY144492; AAO49836.1; -.
NON TER 8
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01-NOV-1999 (TEMBLrel. 12, Created)
01-NOV-1999 (TEMBLrel. 12, Last sequence update)
Nuclear LIM interactor (Fragment).
                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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(TrEMBLrel. 10, Last sequ
(TrEMBLrel. 24, Last anno
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                                                      PRT;
                                                                                                                                                                                                                                                                          Enterobacteriaceae; Salmonella.
NCBI_TaxID=28144;
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Best Local Similarity 40.0%;
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Guery Match
Best Local Similarity 50.vv,
Then 2, Conservative
                                                   PRELIMINARY;
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1 MPITN 5
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01-MAY-1999 (
01-JUN-2003 (
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Q16468;
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Q849P4;
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Wydner K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;
Wydner K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;
The mouse orthologue of the human ionotropic glutamate receptor-like gene (RRINLIA) maps to mouse chromosome 9 ";
U. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

R. EMBL; AF462416; AAO15648.1; -
R. EMBL; AF462416; AAO15648.1; -
R. MGD; MGJ:107282; Grinlia.

R. GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

TON TER 9 9
SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;
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STRAIN-bloom water sample T96-1;
Baker J.A., Entsch B., Neilan B.A., McKay D.B.;
Baker J.A., Entsch B., Neilan B.A., McKay D.B.;
"Monitoring changing toxigenicity of a cyanobacterial bloom using molecular methods.";
Submitted (JN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AX117046; AAM54119.1; -.
NON_TER 8
                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٥,
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Bacteria; Cyanobacteria; Chroococcales; Microcystis.
NCBI_TaxID=198099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                       PRT;
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                                                                                                    PRELIMINARY;
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Best Local Similarity
Matches 3; Conserv
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Plummer N.W., McBurney M.W., Meisler M.H.,
"Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells.",
J. Biol. Chem. 272:34008-24015(1997).

EMBL, U97672; AAB80914.1;
GOS, GOS0007628; Pradult walking behavior; IMP.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                 "The purification of a Rapl GTPase-activating protein from bovine brain cytosol.";
J. Biol. Chem. 267:1546-1553 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
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0
                             SEQUENCE.
MEDLINEs2112868; PubMed=1309786;
MICO E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
Burgess A.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.0%; Score 16; DB 11; Length 9; 75.0%; Pred. No. 1e+06;
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Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                       Length 9;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                            9 AA; 1063 MW; 89EDA77B47604B5A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=RIII; MEDLINE=97442476; PubMed=9295353; Medline=97442476; PubMed=9295353;
                                                                                                                                                                        Query Match
Best Local Similarity 50.0%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STP6 protein (Fragment).
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                                                                                                                                                                                                                                              3 VPLTSV B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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1 VPLS 4
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NCBI_TaxID=1308;
   NCBI_TaxID=9913;
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NON TER
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Q56140
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                                                                 [1] -
SEQUENCE FROM N.A.
MEDLINE-96435920; PubMed-8838806;
James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J.,
Anand R.;
"Walking, cloning and mapping with YACs in 3q27. Localisation of 5
"Walking, cloning and fine Cystatin gene family and
                                                                                                                                      "Walking, cloning and mapping with YACs in 3q27. Localisation of 5 ESTs including 3 members of the Cystatin gene family and identification of CpG islands."; Genomics 32:425-430(1996).

EMBL; X88976; CAA61407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ol-mar-2000 (TrEMBLrel. 13, Last sequence update)
Ol-UN-2002 (TrEMBLrel. 21, Last annotation update)
GAP-3, GTPase-activating protein (Fragment).
Bos taurus (Bovine).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

"Tranformation event-specific quantitative real-time PCR for genetically modified Btl1 maize (Zea mays) and estimation of the Impact of exogenous DNA on the limit of quantification.";

Submitted (JUN-2002) to the EMEL/GenBank/DDBJ databases.

EMBL; AX123624; AAM89275.1; ...
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                                                                                                                                                                                                                                                          32.0%; Score 16; DB 4; Length 8; 100.0%; Pred. No. 1e+06; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                               8 AA; 925 MW; FD5411A7376871E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA; 909 MW; 6046C1B2D77412D7 CRC64;
cosmid cC13-1134 PCR primer 1 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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Best Local Similarity 40.0%;
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Best Local Similarity 100.v.
3; Conservative
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             Homo sapiens (Human).
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                                                     NCBI_TaxID=9606;
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SEQUENCE
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                           STRAIN=STI1;

MUSICALE -95047254; PubWed=7958782;

Constable A., Mollet B.;

Tisolation and characterisation of promoter regions from Streptococcus thermophilus.";

FRMS Microbiol. Lett. 122:85-90(1994).

EMBL; X78210; CAAS5045.1; -.

NON TER

SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

O'Brien M.M., Quinn C.J., Wilson P.G.;

O'Brien M.M., Quinn C.J., Wilson P.G.;

Wolecular Systematics of the Leptospermum Suballiance (Myrtaceae).";

Aust. J. Bot. 48:0-0 (2000).

EMBL; AF184690; AAF03860.1; -.

GO; GO:0009507; C:chloroplast; IEA.

Chloroplast.

B

SEQUENCE 8 AA; 876 MW; ECAIB1B764405056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leptospermum erubescens.
Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myttales, Myttaceae, Leptospermum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.0%; Score 15; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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SEQUENCE FROM N.A.
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ATPB.
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Q9TKES;
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Search completed: March 8, 2004, 12:19:46 Job time : 35.5 secs

5 PTTS 8

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein 8, 2004, 12:11:17; Search time 48.5 Seconds (without alignments) 52.431 Million cell updates/sec March Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-761-636A-10 50 1 CSVPLTSVC 9 Scoring table: score: Sequence:

1586107 seqs, 282547505 residues Searched: 231240 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* A_Geneseq_29Jan04:* 1: geneseqp1980s:* Database

... 8:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aau04529 VEGF base	Abj04424 Stem cell	Abg34948 Human bon	Abj37356 G-protein	Abj37436 G-protein	Abb05266 Vascular	Adc44660 Endotheli	Aaw45666 HBV X 69		Abp54842 Alpha-IIb		_		Abp54835 Alpha-IIb		4		Abj04484 HUVEC cel	Aay48844 Membrane	Aay64300 Cadherin-	Aau03747 Cyclic pe	Abj04620 Bone marr	Bone	Abj04417 Stem cell	Adc44658 Endotheli
ΙD	AAU04529	ABJ04424	ABG34948	ABJ37356	ABJ37436	ABB05266	ADC44660	AAW45666	AAY46691	ABP54842	ADB79677	AAU03756	ABP54826	ABP54835	ABP54823	ABR75294	AAB51972	ABJ04484	AAY48844	AAY64300	AAU03747	ABJ04620	ABJ04630	ABJ04417	ADC44658
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% Query Match	100.0	74.0	64.0	0.09	0.09	60.09	56.0	54.0	54.0	54.0	52.0	52.0	52.0	52.0	52.0	52.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
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Ade78117 Synthetic	Ade78037 Synthetic	Ade78097 Synthetic	Ade77841 Synthetic	Aae05003 Human rel		Aay84175 Amino aci	Aau04530 VEGF base	Aar36888 Insulin-l	Aar43632 Peptide d	Aau03758 Cyclic pe	-	Aau03770 Cyclic pe	Aau03739 Cyclic pe	Aau03760 Cyclic pe	Abg35053 Endostati	Abg68159 Optimised			Abp54837 Alpha-IIb
9 7 ADE78117	9 7 ADE78037	9 7 ADE78097	9 7 ADE77841	6 4 AAE05003	6 4 AAB60620	7 3 AAY84175	7 4 AAU04530	9 2 AAR36888	9 2 AAR43632	9 4 AAU03758	9 4 AAU03731	9 4 AAU03770	9 4 AAU03739	9 4 AAU03760	9 5 ABG35053	9 5 ABG68159	9 5 ABJ04372	9 5 ABP54841	9 5 ABP54837
25 50.0	25 50.0	25 50.0	25 50.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0	24 48.0
26	27	28	29	30	31	32	33	3.4	35	36	37	38	3.9	40	4.	42	43	44	45

ALIGNMENTS

RESULT 1

Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. AAU04529 standard; peptide; 9 AA. VEGF based monocyclic peptide 7. (first entry) 26-SEP-2001 AAU04529; AAU04529

Location/Qualifiers Key Digulfide-bond Synthetic.

/note= "This bond cyclises the peptide"

WO200152875-A1 26-JUL-2001. 18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES

Cendron A;

Stacker S,

Hughes RA,

Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human vegFp (vescular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet a carbon separation distances on opposite antiparallel strands of a

; 0 BRASIL; targeting peptide; bacterial infection; biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes; inflammatory arthritis; arherosclerosis; cancer; autoimmune disease; viral infection; cardiovascular disease; degenerative disease. Identification of targeting peptides that can be used to treat diseases e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis of Selective Ligands) method comprises a single differential Gaps . 0 Length 9; 100.0%; Score 50; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; tive 0; Mismatches 0; Indels Stem cell (mesenchymal) targeting peptide 13. ABJ04424 standard; peptide; 9 AA. 08-SEP-2000; 2000US-0231266P, 17-JAN-2001; 2001US-00765101. 07-SEP-2001; 2001WO-US028124 (TEXA) UNIV TEXAS SYSTEM. (first entry) Conservative Arap W, Pasqualini R; 1 CSVPLTSVC 9 6 WPI; 2002-404697/43. diabetic retinopathy Local Similarity les 9; Conserv CSVPLTSVC WO200220822-A2 Sequence 9 AA; Unidentified. 24-OCT-2002 14-MAR-2002. ABJ04424; Query Match Best Loca Matches RESULT 2 ABJ04424 \$ à

Example 5; Page 75; 167pp; English.

centrifugation step.

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of Selective Interactive Ligands) to obtain a targeting peptide. The BRASIL method of the invention involves: exposing a target to a phage display library in a first phase; exposing the first phase to a second phase; and separating the phage bound to the target from unbound phage. The BRASIL method of the invention allows cell phases to be separated from the remaining unbound phage in a single differential centrifugation step. When compared to conventional cell panning methods, the BRASIL method shows a significant increase in recovery of specific phage and a substantial decrease in Dackground. The BRASIL method is useful for cidentifying targeting peptides. The targeting peptides identified by the combination are useful for treating disease states, such as:

CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune degenerative disease. The present amino acid sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to a novel method for identifying disease targeting peptides. The method comprises exposing a sample from an organ, tissue or cell type of interset, to a phage display library and recovering phage bound to the sample (the phage expresses targeting peptides). The peptides identified by the method of the invention may
invention comprises a method (BRASIL - Biopanning and Rapid Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Targeting peptide; cancer; Hodgkin's disease; cytostatic; immunosuppressive; anti-inflammatory; antiarthritic; antiviral; antiatherosclerotic; antidiabetic; antidiabetic; dispetes mellitus; inflammatory disease; arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Score 3/; ____Pred. No. 1.4e+06; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                74.0%; Score 37; DB 5; Length 9; 66.7%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human bone marrow targeting peptide #20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 56; Page 207; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG34948 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-SEP-2001; 2001WO-US027702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-2000; 2000US-0231266P.
17-JAN-2001; 2001US-00765101.
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                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200220722-A2.
                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2002.
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ABG34948
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                                                                                                                                                                                                                                                                                                                                                  ö
               antiatherosclerotic, antidiabetic, antibacterial and antivital activities. The methods and composition are useful for identifying targeting peptides and one or more receptors for a targeting peptides. The targeting peptides are used for selective delivery of therapeutic agents, including gene therapy vectors and fusion proteins, to specific organs, tissues, or cell types in subject. The targeting peptide may also be used for treating diseases such as diabetes mellitus, inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and viral infections and Hodgkin's disease. The present sequence represents a targeting peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing compound library, by generating biological target model using target sequence information, defining microenvironments interacting with ligand and motifs interacting with microenvironment, and assembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compound library; microenvironment; G-protein Coupled Receptor; GPCR.
cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                    Score 32; DB 5; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-protein coupled receptor peptide region #68.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABJ37356 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                    64.0%;
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                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      CSPPLTRWC
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                                                                                                                                                                                                                                                                  Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JAN-2003.
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ABJ37356
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Sequence 7 AA;

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                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing compound library, by generating biological target model using target sequence information, defining microenvironments interacting with ligand and motifs interacting with microenvironment, and assembling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G-protein coupled receptor endothelin ET-A receptor peptide #68.
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Score 30; DB 6; Length 7;
Pred. No. 1.4e+06;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                  ABJ37436 standard; peptide; 7 AA.
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     60.0%;
83.3%;
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                                                             5; Conservative
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                                                                                                                     1 CSVPLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified.
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Unidentified.
           25-OCT-2001.
 29-AUG-2003
04-APR-2002
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The present invention describes a method for screening a ligand library (IL). The method comprises: (a) contacting the IL with an anti-target (AT) to allow the ligands to bind to the AT; (b) separating unbound ligands; (c) contacting the unbound ligands with a selected target (T) to allow binding of unbound ligands to (T) to form a (T)-bound ligand complex (C); (d) separating (C) from ligands which do not bind (T); and (C) id separating (C) from ligands which do not bind (T); and (C) id separating (C) from ligands which do not bind (T); and (C) id separating (C) from ligands which do not bind (T); and (C) id serion a ligand library, e.g., a library of peptides, polypeptides, non-polypeptides or oligonucleotides. A ligand (I) identified by the application. The method is preferably useful for identified by the application. The method is preferably useful for identifying peptides useful in cleaning compositions, which involves contacting peptides useful in cleaning compositions, which involves contacting peptides useful in cleaning compositions, which involves contacting peptides with a target which is a stain such as porphyrin derived stain, tannin derived stain, and soil-based derived stain, and peptide complex and identifying the stain-bound peptide complex. A selective manner of the stain-bound peptide complex. A selective manner 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             method may be used to identify cell type specific surface molecules. Preferred anti-targets include one or more different cell types, cells in different stares, or cells that do not display the surface molecule. ABB05322 to ABB0546 represent phage-peptides ligands which are used in the exemplification of the present invention. (Updated on 29-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Screening ligand library comprises allowing binding of ligand with antitarget, contacting unbound ligands with selected target to form target-bound ligand complex and identifying target bound ligands on the complex.
                                                                                                                                                                                                                                                                                                      Human; tumour necrosis factor alpha; TNP-alpha; VEGF; detergent; stain; bacteriophage; phage library; vascular endothelial growth factor; collar soil; polyurethane; egg; tea; hair; skin; cleaning composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  identify ligands that bind to a target under harsh conditions. The selective targeting method may be used to screen and identify a ligand useful for therapeutic intervention, e.g., a library of ligands may be screened to identify a tumour-bound ligand. The selective targeting
                                                                                                                                                                               Ascular endothelial growth factor binding peptide V-20 SEQ ID NO:98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-APR-2000; 2000US-0197259P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified bacteriophage.
(revised)
(first entry)
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The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell peptide or polypeptide which includes one or more endothelial cell binding protein (ECBP) sequences. A peptide of the invention has anticomputation, vasotropic, antipsoriatic, dermatological, antidiabetic, antiatrbritic, valnerary, antiulcer, coptibalmological, antidiabetic, antiatrbritic, valnerary, antiulcer, antinflammatory, antibacterial, and gynaecological activity. The peptide of antinflammatory, reducing the proliferation and/or migration of complete lal cells, by treating the cells with an ECBP agonist, which is conforbelial cells, by treating the cells with an ECBP antagonist, which is preferably the peptide of the invention and/or migration of the invention. A peptide of the invention is also useful for manufacturing a medicament for promoting angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing angiogenesis. ECBP antagonise the present sequence represents an ECBP of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel synthetic or recombinant polypeptide useful for promoting, reducin proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.
                                                                                                                                                                                               endothelial cell binding protein; ECBP; anti-tumour; cytostatic; vasotropic; antipsoriatic; dermatological; ophthalmological; antidiabetic; antiarthritic; vulnerary; antiulcer; antinflammatory; antibacterial; gynaecological; anglogenesis.
                                                                                                                                                             Endothelial cell binding peptide SEQ ID NO:389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsaioun K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 389; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morris AJ,
                                          ADC44660 standard; peptide; 9 AA.
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                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GPCB-) GPC BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lamphere L,
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                                                                                                                         18-DEC-2003
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                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                                  ADC44660;
RESULT 7
ADC44660
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Gaps

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56.0%; Score 28; DB 7; Length 9; 33.3%; Pred. No. 1.4e+06; ive 3; Mismatches 3; Indels

Conservative

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Query Match

Sequence 9 AA;

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AAW45666 RESULT

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60.0%; Score 30; DB 5; Length 9; 44.4%; Pred. No. 1.4e+06; ive 2; Mismatches 3; Indels

Query Match Best Local Similarity 44.4%;

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Matches

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01-DEC-1999 (first entry)
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                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                    WO9945954-A1.
                                                                                                                                                                                                                                                                                                                                            13-MAR-1998;
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                                                                                                                                                                                                                                                                                                        6-SEP-1999
                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents an immunogenic peptide with binding affinity for HLA-A3-like molecules. A cytotoxic T cell (CTL) response against a HLA-A3-like molecules. A cytotoxic T cell (CTL) response against a namenogenic peptide (Ag) is induced in a patient by contacting a CTL with an immunogenic peptide of 9-15 amino acids which binds to at least two HLA-A3-like molecules with dissociation constant less than 500 mM and induces a cytotoxic T cell response. The immunogenic peptide has a sequence of 9 amino acids, comprising a binding motif, with from the N-to C-termin: primary anchor sites (PAR) at positions 2 (selected from Ala, Leu, Ile, Val, Met, Ser or Thr) and 9 (Arg or Lys) and at least one secondary anchor sites (SAR), i.e. Tyr, Phe or Trp at positions 3, 6 or 7, and/or Pro at position 8. The immunogenic peptides are used in peptide based vaccines and therapeutic compositions, for treating viral, parasitic or fungal diseases or cancer, e.g. prosetatic cancer, hepatitis B or condyloma acuminatum. They can also be used to elicit a CTL response or condyloma cuminatum. They can also be used to elicit a CTL response to in vitro for subsequent respond to peptide vaccines or other therapies.

The patient does not respond to peptide vaccines or other therapies.

The patient does not respond to Peptide vaccines or other therapies.

The patient does not respond to Peptide vaccines or other therapies.

The patient does not respond to Peptide vaccines or other therapies.
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                                                                                                                                                                HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity; HLA-A3 supermotif; tumour; infection; parasite; CTL; antigen, HIV pol; HBV; hepatitis b virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inducing cytotoxic T cell response against specific antigen - using immunogenic peptide with binding affinity for HLA-A3-like molecules, treat or prevent tumours and infections by virus, parasites etc.
                                                                                                                                HBV X 69 peptide with binding affinity for HLA-A3-like molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.0%; Score 27; DB 2; Length 9; 57.1%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 37; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY46691 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sidney J;
    AAW45666 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                        97WO-US003778.
                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0013113P.
                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sette A, Chestnut RW,
                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-470637/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CALPFTS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   correct OS field.)
                                                                                                                                                                                                                                                      Synthetic.
Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1996;
                                                                                                                                                                                                                                                                                                              WO9733602-A1
                                                                                                                                                                                                                                                                                                                                                  18-SEP-1997.
                                                                            27-AUG-2003
09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY46691;
                                          AAW45666;
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AAY46691 ID AAY4 XX AC AAY4

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AXY AAY45390 to AAY48214 represent specifically claimed immunogenic peptides can baving a human major histocompatibility complex (MHC) Class I (also known as human leukcyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, Al. A3.2 cor A24.1 or HLA-B or C) and induce a cytocoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes cor A24.1 or HLA-B or C) and induce a cytocoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes correctly may be a contained by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intext foreign antigen itself, and are particularly important in antigen and in fighting viral infections. The peptides are concers in mammals (especially to treat or prevent viral infections and cancers in mammals especially humans) e.g. prostate cancer, hepatitis B concers in immunity cancer in minimisers in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to indice claim expanse, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a concert cuseful therapeutically and for immunisation as above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·.
mmunogenic peptide having a human leukocyte antigen binding motif #1302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                               Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sette A, Kubo RT, Sidney J, Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP54842 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 81; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US005039.
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Guery Match
Best Local Similarity 57.13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-551214/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSVPLTS 7
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viral infections, non-viral infections, proliferative disease; inflammatory disease, allergic disease; autoimmune disease.
                                                                                                                                                        12-JUN-2002; 2002WO-EP006440.
                                                                                                                                                                                       13-JUN-2001; 2001NZ-00512341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                       WPI; 2003-221750/21.
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                                                                                                                                                                                                                        (FARB ) BAYER AG.
                                                                                           WO2003006654-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001
                                                          Parapoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                        23-JAN-2003.
                                                                                                                                                                                                                                                                          Fleming SB;
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                                                                                                                                                                                                                                                                                                                                                                                           di sease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a novel alpha-IID beta-3 integrin (glycoprotein IID/IIIa or CD41/CD61) activating peptide. This cyclic peptide comprises a consensue binding mocif (Val-Pro-Trp) and was identified by focusing a phage library screening on integrin ligands which are not blocked by a GRGDS peptide. The VPW motif is present in the A3-domain of von Willebrand factor (VWf), suggesting that VMf is an interaction. The invention relates to the use of novel peptides (see ABP54823-25) comprising the consensue binding motif as pharmaceuticals for the treament of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New alphaIIb beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue regeneration.
                                                                                                                                                                                           /note= "binding motif, region specifically described in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        virucide; anti-HIV; hepatotropic; antiinflammatory; cytostatic; vulnerary; antiatasthmatic; antialiergic; dermatological; antidiabetic; immunosuppressive; antitrheumatic; antiarthritic; thyromimetic; protozoacide; amoebicide, antibacterial; gene therapy; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                            Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 5; Length 9;
Pred. No. 1.4e+06;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                               (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
             Alpha-IIb beta-3 integrin activating peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parapoxvirus ORF 100 C-terminal peptide.
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 12; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB79677 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.0%;
                                                                                                                                                                                                                                                                                                                12-MAR-2002; 2002WO-FI000193.
                                                                                                                                                                                                                                                                                                                                              12-MAR-2001; 2001FI-00000492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Koivunen E, Gahmberg CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSVPLTSVC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                  WO200272619-A1.
                                                                                                                                                                                                                                                                                  19-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB79677;
                                                                                                                   Synthetic.
                                                                                     cyclic.
                                                                                                                                                                                      Region
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The invention relates to a novel purified and isolated polymucleotide c((NI) of Parapoxvirus ovis (PPVO) comprising a nucleotide sequence (SI, or defined in the specification). Or its complementary sequence, fragment or functional variant. A polymucleotide of the invention has virucide, anti-HIV, hepatotropic, anti-Hiflammatory, cytostatic, virucide, anti-HIV, hepatotropic, hereafted prima virus polymucleotides, or recombinant viruses comprising a Vaccinia virus polymucleotides, or recombinant viruses comprising a Vaccinia virus paper or influences, herpes virus infections, inversible (e.g. hepatitis, papillomatosis, herpes virus infections, infections or influence, virus infections, non-viral infections (e.g. cancer, leukaemia, warrs or other skin proliferative disease (e.g. cancer, leukaemia, warrs or other skin coplasms), inflammatory disease (e.g. Crohn's disease, Coppiasms), inflammatory disease (e.g. Crohn's disease, conditions related to healing of wounds), allergic disease, and/or autoimmune diseases (systemic lupus erythematosus, Sjogren's disease, coppiance is used in the exemplification of the invention.
                                                                                                                                                                                                                                                          New polynucleotide and recombinant proteins of Parapoxvirus ovis, useful for manufacturing a medicament for treating virus related disease, viral infections, non-viral infections, proliferative disease or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
;
Schlapp T, Mercer AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cyclic peptide inhibitor of LFA-1/ICAM-1 interaction #33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.0%; Score 26; DB 7; Length 7; 66.7%; Pred. No. 1.4e+06; ive 1; Mismatches 1; Indels
           Friederichs SM, Siegling A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; Page 37; 51pp; English.
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The present sequence is that of a novel alpha-IIb beta-3 integrin (glycoprotein IIb/IIIa or CD41/CD61) activating peptide. This cyclic peptide comprises a consensus binding motif (Val-Pro-Trp) that was identified by focusing a phage library screening on integrin ligands, which are not blocked by a GRODS peptide. The motif is present in the A3-domain of von Willebrand factor (VWf), suggesting that VWf is an activator of the alpha-IIb beta-3 complex, enabling stable platelet-VWf interaction. The invention relates to the use of novel peptides comprising the consensus binding motif as pharaceuticals for the treatment of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)
                                                                                                                                                                            New alphaIIb beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "binding motif, region specifically described in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.0%; Score 26; DB 5; Length 9; 44.4%; Pred. No. 1.4e+06; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-IIb beta-3 integrin activating peptide.
                                                                                                    (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                          Disclosure; Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP54835 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2002; 2002WO-FI000193.
                                                                         12-MAR-2001; 2001FI-00000492.
                                           12-MAR-2002; 2002WO-FI000193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                     Koivunen E, Gahmberg CG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSVPLTSVC 9
                                                                                                                                                                  WPI; 2002-750482/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:||
CAVPWARYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JAN-2003
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                19-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP54835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó;
                                                                                                                                                                                                                                                                                                                                                                                                    The sequence represents the amino acid sequence of cyclic peptide inhibitor #33 of lymphocyte function associated antigen-1 and intracellular adhesion molecule (LFA-1/ICAM-1) interaction. A composition comprising a cyclic peptide inhibitor of LFA-1/ICAM-1 interaction is useful for treating haematopoietic neoplastic disease, myocardial infarction, radiation injury, asthma, rhemanciod arthrits or lymphoma metastasis. The composition is also useful for inhibiting in a subject the interaction between LFA-1 expressed on a leukocyte and ICAM-1 expressed on another cell, preventing retinoic acid syndrome in a subject receiving all-trans retinoic acid, inhibiting growth of leukaemia cells, inhibiting drowth of leukaemia cells, a candidate compound for binding to ICAM-1
                                                                                                                                                                                                                                                                                                           Composition comprising a cyclic peptide inhibitor of lymphocyte function associated antigen-1 and intracellular adhesion molecule 1 interaction, for treating e.g. asthma and myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3. 5
/note= "binding motif, region specifically described in
Claim 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary; cyclic.
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radiation injury; rheumatoid arthritis; lymphoma metastasis; retinoic acid syndrome; all-trans retinoic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.0%;
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16-JAN-2001; 2001US-00760599.
                                                                                                                                           16-JAN-2001; 2001WO-US001382.
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Gaps

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The present sequence is that of a novel alpha-IID beta-3 integrin (glycoprotein IID/IIIa or CD41/CD61) activating peptide. This cyclic peptide comprises a consensus binding motif (Val-Pro-Trp) and was identified by focusing a phage library screening on integrin ligands which are not blocked by a GROB peptide. The VPW motif is present in the A3-domain of von Willebrand factor (VWf), suggesting that VMf is an interaction. The invention relates to the use of novel peptides (see ABP54823-25) comprising the consensus binding motif as pharmaceuticals for the treament of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)

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/note= "binding motif, region specifically described in
Claim 1"

                                                                                             New alphalib beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-IIb beta-3 integrin activator; integrin; CD41; CD61; glycoprotein IIb/IIIa; von Willebrand disease; coagulant; vulnerary;
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44.4%; Pred. No. 1.4e+06;
tive 2; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alpha-IIb beta-3 integrin activating peptide.
           (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
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                                                                                                                                                                                Disclosure; Page 12; 34pp; English.
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Matches 4; Conserv
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Search completed: March 8, 2004, 12:17:51 Job time : 49.5 secs

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The present sequence is that of a novel alpha-IIb beta-3 integrin (glycoprotein IIb/IIIa or CD41/CD61) activating peptide. This cyclic peptide comprises a consensus binding motif (Val-Pro-Trp) that was identified by focusing a phage library screening on integrin ligands, which are not blocked by a GRODS peptide. The motif is present in the A3-domain of von Willebrand factor (VWF), suggesting that VWF is an interaction. The invention relates to the use of novel peptides interaction. The invention relates to the use of novel peptides comprising the consensus binding motif as pharaceuticals for the recatnent of thrombotic diseases and bleeding disorders, including von Willebrand disease, and in artificial tissue transplants to aid in wound healing and tissue regeneration (all claimed)
                                                                                                                                          New alphalIb beta3 integrin activating peptides useful for manufacturing a composition for treating or preventing thrombotic or bleeding disorders, e.g. von Willebrand disease, and in wound healing and tissue regeneration.
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Pred. No. 1.4e+06;
0; Mismatches 5; Indels
                                              (CTTC-) CTT CANCER TARGETING TECHNOLOGIES OY.
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           12-MAR-2001; 2001FI-0000492.
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Query Match
Best Local Similarity 44.4%,
                                                                                     Gahmberg CG;
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2: /cgu2_6/ptodata/2/pubpaa/NCT_NEW_PUB.pep:*
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3: /cgu2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. 1 2 3 3 4 4 4 4 6 6 10 11	SCOTE 2007 2007 2007 2007 2007 2007 2007 200	% Match Match 100.0 100.0 55.0 55.0 55.0 50.0 50.0 50	Attch Length DB fatch Length DB for 0 9 9 9 60.0 9 14 55.0 9 9 14 55.0 9 9 14 50.0 9 14 48.0 9 9 15 50.0 9 14 8.0 9 9 15 50.0	DDB 99 114 115 115	ID US-09-761-636A-10 US-09-832-723-98 US-10-303-331-98 US-10-26-457-389 US-10-254-446A-147 US-09-760-599-34 US-10-254-446A-147 US-09-760-599-25 US-10-06-869-3514 US-10-286-457-387 US-09-761-636A-11 US-09-761-636A-11 US-09-761-636A-11	Description Sequence 10, Appl Sequence 98, Appl Sequence 98, Appl Sequence 389, Appl Sequence 34, Appl Sequence 147, Appl Sequence 3614, Ap Sequence 3614, Appl Sequence 3614, Appl Sequence 3614, Appl Sequence 11, Appl
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RESULT 2 US-09-812-723-98 ; Sequence 98, Application US/09832723 ; Patent No. US20020098524A1

38,	Sequence 48, Appl	e 6, Ag	284,	equence 249,	322,		464,	equence 249,	322,	349,	464,		256,	257,		792,	808	1314	e 1319	1344	e 1857	1864	e 1882	382	2409	2411	2917	2943	Semience 2948. An	}
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ALIGNMENTS

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Sequence 10, Application US/09761636A

Patent No. US20020065218A1

Sequence 10, Application US/09761636A

Patent No. US20020065218A1

SEQUENCEAL INCREMATION:

APPLICANT: STACKER, Steven

APPLICANT: STACKER, Steven

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

APPLICANT: HUGHES, Richard

CURRENT FILING DATE: 2001-01-18

FRIOR PILING DATE: 2001-01-18

PRIOR PLICATION NUMBER: US 60/176,293

PRIOR PLICATION NUMBER: US 60/176,293

PRIOR PLICATION NUMBER: US 60/204,590

PRIOR PLICATION NUMBER: US 60/204,590

PRIOR PRIOR FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin version 3.0

SEQ ID NO 10

LENGTH: 9

TYPE: PRT

CREANISM: Homo sapiens

US-09-761-636A-10

Query Match

Best Local Similarity 100.0%; Score 50; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.2e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0;

COPPLICATOR

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TYPE: PRT
ORGANISM: Artificial Sequence
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60.0%; Score 30; DB 9; Length 9;
Best Local Similarity 44.4%; Pred. No. 7.2e+05;
Matches 4; Conservative 2; Mismatches 3; Indels
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Publication No. US200301529f6A1

GENERAL INFORMATION:

APPLICANT: Janssen, Giselle G.

APPLICANT: Minetzky, Deborah S.

TILLE REFERENCE: GC617-3

FILLE REFERENCE: GC617-3

CURRENT APPLICATION NUMBER: US/10/303,331

CURRENT FILING DATE: 2002-11-25

PRIOR APPLICATION NUMBER: US 09/832,723

PRIOR APPLICATION NUMBER: US 09/832,723

PRIOR PILING DATE: 2000-04-11

PRIOR PILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 125

SOFTWARE: FRACESQ for Windows Version 4.0
GENERAL INFORMATION:
APPLICANT: Estell, David A.
APPLICANT: Chen, Yiyou
APPLICANT: Mixray, Christopher J.
APPLICANT: Tijerina, Pilar
TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
FILE REPERENCE: GG617-2
CURRENT APPLICATION NUMBER: US/09/832,723
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/197,259
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 117
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 389, Application US/10286457; Publication No. US20030166004A1; GENERAL INFORMATION:
APPLICANT: JENO GYURIS et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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1 CKMPTSKVC 9
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US-10-286-457-389
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                                                                                                                                                                                                                                                                                     SEQ ID NO 98
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; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, base; OTHER INFORMATION: ability to selectively bind to endothelial cells US-10-286-457-387
                                                                                                                                                                             Sequence 387, Application US/10286457
Fublication No. US20030166004A1
GENERAL INFORMATION:
APPLICANT: JENO GYURIS et al.
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REPRENCE: GPCT-P0-178
CURRENT APPLICATION NUMBER: US/10/286,457
CURRENT PILING DATE: 2002-11-01
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
SOFTWARE: Patentin version 3.1
LENGTH: 9
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**Publication No. US20030229199A1

**GENERAL INVORMATION:

**APPLICANT: Symonds, Jonest W.

**APPLICANT: Symonds, Jonest W.

**TILE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL

**TILE OF INVENTION: CADRENTA MEDIATED FUNCTIONS

**TILE REFERENCE: 100086.497C9

**CURRENT PILICATION NUMBER: US/10/395,032

**CURRENT PILICATION NUMBER: 2003-03-21

**NUMBER OF SEQ ID NOS: 4052

**SEQ ID NO 3614

**LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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1 CTFHIDSVC
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                                                                    ; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopan
US-10-254-446A-147
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| Sequence 3614, Application US/10006869
| Sequence 3614, Application US/10006869
| Publication No. US_20030082166A1
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Ones Watthew
| APPLICANT: Symonds, James Matthew
| APPLICANT: Gour, Barbara J.
| TITE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
| TITE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
| FILE REFERENCE: 100086,40777
| CURRENT APPLICATION NUMBER: US/10/006,869
| CURRENT APPLICATION NUMBER: US/10.12-03
| NUMBER OF SEQ ID NOS: 4052
| SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                             : Sequence 25, Application US/09760599;
Fatent No. US20010034326A1;
GENERAL INFORMATION:
APPLICANT: Larson Mr., Richard S.;
TITLE OF INTURNITOR: Poptide Inhibitors of LFA-1/CAM-1 Interaction;
FILE REFERENCE: SCI200/4-1CIP;
CURRENT FILING DATE: 2001-01-17;
NUMBER OF SEQ ID NOS: 56;
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
) OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-760-599-25
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                                                                                                                                                                Query Match 52.0%; Score 26; DB 14; Length 9; Best Local Similarity 44.4%; Pred. No. 7.2e+05; Matches 4; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.0%; Score 25; DB 9; Length 9; Best Local Similarity 33.3%; Pred. No. 7.2e+05; Matches 3; Conservative 3; Mismatches 3; Indels
                         TYPE: PRT ORGANISM: artificial sequence
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LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Largeon Mr., Richard S.
TITLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
FILE REFERENCE: SCI200/4-LGIP
CURRENT APPLICATION NUMBER: US/09/760,599
CURRENT FILING DAIR: 2001-01-17
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 9
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Patent No. US20010034326A1
GENERAL INFORMATION:
APPLICANT: Larson Mr., Richard S.
TILLE OF INVENTION: Peptide Inhibitors of LFA-1/CAM-1 Interaction
FILE REFERENCE: SCI20/4-1.CIP
CURRENT APPLICATION NUMBER: US/09/760,599
CURRENT PILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Patentin Ver. 2.1
LENGTH: 9
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                                                                                                                                Query Match
48.0%; Score 24; DB 8; Length 9;
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels
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Patent No. US20010034326Al
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Best Local Similarity 33.34
Matches 3; Conservative
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1 CLLRMNSIC 9
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1 CMLRMRSIC 9
                    TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-344-824-293
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STRANDEDNESS:
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US-09-760-599-17
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US-09-760-599-9
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     Sequence 11, Application US/09761636A
Fatent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACKEN, Marc
APPLICANT: ACKEN, Marc
APPLICANT: CRUDRON, Angela
ITILE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPREMEE: 1064/48E5 C01-01-18
FILE REPREMEE: 2001-01-18
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-01-16
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 11
FROM A PAREMEE A PAREMEE SUPPLICATION NUMBER: US 60/204,590
PRIOR APPLICATION VUMBER: US 60/204,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 299, Application US/08344624
) Publication No. US20030152580A1
) GENERAL INFORMATION: US20030152580A1
) APPLICANT: SETTE, Alessandro
APPLICANT: SIDNEY, John
) TILLE OF INVENTION: HitA BINDING PEPTIDES AND THEIR USES
) NUMBER OF SEQUENCES: 399
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND Khourie and Crew
) STREET: Ploor

STREET: Ploor
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION STATE
APPLICATION NUMBER: US/08/344,824
FILING DATE: 12-UUL-1994
ATTOMNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 14,774
REFERENCE/DOCKET NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
METERNOR (ACCOUNT NUMBER: 14137-80-1
TELECOMMUNICATION INFORMATION:
METERNOR (ACCOUNT NUMBER: 14137-80-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 293:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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Best Local Similarity 100.0
Matches 5; Conservative
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STATE: California
COUNTRY: USA
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ORGANISM: Homo sapiens
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36, Appl 256, Appl 11, Appl 3663, Ap 3663, Ap 985, App 2242, Ap 2242, Ap

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Sequence 3624,
Sequence 1071,
Sequence 3624,
Sequence 36, A
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Fatent No. 609038B
GENERAL INFORMATION:
APPLICANT: WANG, Chang Yi
TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND TITLE OF INVENTION: IMMUNE DISORDERS
TUTLE OF INVENTION: IMMUNE DISORDERS
CORRESPONDENCE ADDRESS:
ADDRESSES: MORGAN & FINNEGAN
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Pred. No. 3e+05;
2; Mismatches 2; Indels
US-09-258-754-256
US-09-042-107-36
US-09-042-107-48
US-09-187-859-1071
US-09-187-859-1071
US-09-1839-5428-3624
US-09-722-2500-36
US-09-722-2500-36
US-09-722-2500-256
US-09-722-2500-256
US-09-722-2500-256
US-09-187-859-3663
US-09-187-859-3663
US-09-187-859-985
US-09-187-859-985
US-09-187-859-985
US-09-187-859-985
US-09-187-859-985
US-09-187-859-985
US-09-839-5428-3663
US-09-839-5428-3663
US-09-839-5428-3663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: NY
COUNTRY: NY
ZIP: 10154-0054
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,409A
FILING DATE
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151-4154
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REFERENCE/DOCKET NUMBER: 1151
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.2%;
50.0%;
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New York
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Best Local Similarity
Matches 4; Conserv
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   US-09-100-409A-27
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CITY: N
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70, Appl

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72, Appl

73, Appl

74, Appl

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76, Appl

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77, Appl

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                                                                                                               March 8, 2004, 12:00:45; Search time 22 Seconds (without alignments) 18.773 Million cell updates/sec
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// /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
// /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
// /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
// /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
// /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
// /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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S-09-839-542B-3664
S-09-187-859-3665
S-09-839-542B-3665
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US-09-62-107-49

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US-09-72-250D-49

US-08-73-551-14

US-08-73-551-14

US-09-079-432-3

US-09-079-432-3

US-09-079-432-3

US-09-079-432-3

US-09-079-107-33

US-09-042-107-214

US-09-122-250D-33

US-09-722-250D-33

US-09-722-250D-33

US-09-122-250D-33

US-09-122-250D-34

US-09-122-250D-34

US-09-122-250D-34

US-09-122-250D-34

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US-09-122-250D-34

US-09-122-250D-34

US-09-122-250D-34

US-09-1287-850B-3664
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US-09-258-754-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                     using sw model
                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                           US-09-761-636A-6
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Match Length
                                                                                     protein search,
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                                                                                                                                                                                                                                                             BLOSUM62
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Perfect score:
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| GENERAL INFORMATION:
| APPLICANT: Rucelahri, Erkki
| APPLICANT: Radjotte, Daniel
| APPLICANT: Radjotte, Daniel
| APPLICANT: Radjotte, Daniel
| TITLE OF INVENTION: Methode of Identifying Lung Homing Molecules Using
| TITLE OF INVENTION: Methode of Identifying Lung Homing Molecules Using
| TITLE OF INVENTION: Methode of Identifying Lung Homing Molecules Using
| TITLE OF INVENTION: Methode of Identifying Lung Homing Molecules
| FILE REPRENTED PRICATION NUMBER: US/09/258,754
| CURRENT APPLICATION NUMBER: US/09/226
| EARLIER FILLING DATE: 1998-03-13
| NUMBER OF SEQ ID NOS: 452
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 49
| LENGTH: 8
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Sequence 49, Application US/09042107

Patent No. 623287

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Tissues

FILE REFERENCE: P-LJ 2892

CURRENT APPLICATION NUMBER: US/09/042,107

CURRENT FILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 436

SOCIED NO 49

LENGTH: 8
                                                                                                      Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-49
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                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.3%; Score 25; DB 3; Length 8; Best Local Similarity 50.0%; Pred. No. 3e+05; Matches 4; Conservative 1; Mismatches 3; Indels
                                               54.3%; Score 25; DB 1; Length 8; 37.5%; Pred. No. 3e+05;
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                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                       Sequence 49, Application US/09258754
Patent No. 6174687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                          Query Match
Dest Local Similarity 37.5%;
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1 CGQSKVIC 8
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US-08-397-633A-100
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                                                                                                              GENERAL INFORMATION:

APPLICANT: Great, Randall G.

APPLICANT: Great, Randall G.

APPLICANT: Great, Randall G.

APPLICANT: Mermer, Brion

TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNOBERICIENCY VIRUS INFECTION

TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNOBERICIENCY VIRUS INFECTION

TITLE OF INVENTION: USING ENV/GAG POLYPEPTIDE MARKERS

FILE REFERENCE: 00088/111001

CURRENT APPLICATION NUMBER: US/09/089, 878

CURRENT FILING DATE: 1998-06-03

EARLIER APPLICATION NUMBER: US 60/085, 615

EARLIER PILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FASTER OF WINDOWS VERSION 3.0

SEQ ID NOS: 3

SEQ ID NOS: 3
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Sequence 100, Application US/08397633A

PERENT NO. 5773577

GENERAL INFORMATION:

APPLICANT: Cappello, Joseph

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 105

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Babarcadero Center, Suite 3400

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.5%; Score 26; DB 4; Length 8; Best Local Similarity 37.5%; Pred. No. 3e+05; Matches 3; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFRENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERA: (415) 388-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTEY: USA

ZIP: 94111-4187

COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Feline immunodeficiency virus
                                       US-09-089-878-3
; Sequence 3, Application US/09089878
; Patent No. 6458528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 amino acids
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
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Patent No. 5817750
GENERAL INFORMATION
GENERAL INFORMATION
FAPPLICANT: Rucelahri, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Plores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 23; DB 2; Length B; 37.5%; Pred. No. 3e+05; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 23; DB 3; Length 7; 80.0%; Pred. No. 3e+05; tive 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPRATING SYSTEM: PC Compatible
OPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,535
FILING DATE: 28-AUG-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFO 309

ATTORNEY AGENT INFO 304

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IA 1794

TELEPHONE: (619) 535-9001

TELEPAX: (619) 535-9001

INFORMATION FOR SEQ ID NO: 3:
33,683
---- 65691/130
        REGISTRATION NUMBER: 33,683
REFERRINCE/DOCKET NUMBER: 65
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity BU.v.,
Acc 4; Conservative
                                                                                                                                                                                                                      TELEX: 904136
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 37.5 Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CNEESLIC 8
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1 CWDDGLMC 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-520-535-3
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AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT A
PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
DIAGNOSIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                  Sequence 49, Application US/09722250D

Sequence 49, Application US/09722250D

Patent No. 6610651

GENERAL INFORMATION:

APPLICANT: Rasqualini, Renata

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Tissues

FILE REPERENCE: P-L4 4514

CURRENT APPLICATION NUMBER: US/09/722,250D

CURRENT APPLICATION NUMBER: US 09/042,107

PRIOR PFILING DATE: 1998-03-13

NUMBER OF SEO ID NOS: 437

SOFTWARE: Patentin Ver. 2.0

TENGRAPH OF SECOND OF S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 54.3%; Score 25; DB 4; Length 8; Best Local Similarity 50.0%; Pred. No. 3e+05; Matches 4; Conservative 1; Mismatches 3; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OERRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,551
FILING DATE: 30-DEC-1997
CLASSIFICATION DATA: APPLICATION DATA:
APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION D
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Chermann, Jean-Claude
APPLICANT: Le Contel, Carole
APPLICANT: Galea, Pascale
TITLE OF INVENTION: VACCINE ACAINST
TITLE OF INVENTION: PREVENTION OF H
TITLE OF INVENTION: DIAGNOSIS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/08973551
Patent No. 6113902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & STREET: 3000 K Str CITY: Washington STATE: D.C. COUNTRY: USA
        1 CGNETLRC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGNETLRC 8
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Gaps

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Sequence 214, Application US/09258754

Sequence 214, Application US/09258754

Patent No. 6174687

GENERAL INFORMATION:
APPLICANT: Rajet, Daniel
APPLICANT: Rajet, Daniel
APPLICANT: Rajet, Daniel
APPLICANT: Rajet, Daniel
APPLICANT: Membrane Dipeptidase
FILE REPERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT APPLICATION NUMBER: US/09/228,754
CURRENT FILING DATE: 1999-0-2-6
EARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                   Sequence 42, Application US/09258754

Sequence 42, Application US/09258754

Sequence 42, Application US/09258754

GENERAL INFORMATION:

APPLICANT: Rucelahri, Erkki

APPLICANT: Rajotte, Daniel

TITLE OF INVENTION: Merhods of Identifying Lung Homing Molecules Using

TITLE OF INVENTION: Membrane Dipeptidase

FILE REFERENCE: P-LJ 3443

CURRENT APPLICATION UNBER: US/09/258,754

CURRENT FILING DATE: 1999-02-26

EARLIER PILING DATE: 1998-03-13

NUMBER OF SEQ ID NOS: 452

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 42
                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-214
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                                                                                             4; Indels
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                                                  Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
                                               Score 23; DB 3;
Pred. No. 3e+05;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 23; DB 3;
50.0%; Pred. No. 3e+05;
tive 1; Mismatches
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ORGANISM: Artificial Sequence
                                                  50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.01
Matches 4; Conservative
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Best Local Similarity 37.54
Matches 3; Conservative
                                             Query Match
Best Local Similarity 50.0
Matches 4; Conservative
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1 CHEGYLTC 8
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    JS-09-258-754-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rucellahri, Erkki
APPLICANT: Ragotalni, Remata
APPLICANT: Ragotalni, Remata
APPLICANT: Pasqualni, Remata
APPLICANT: Rajotte, Daniel
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
TITLE OF INVENTION: Membrane Dipeptidase
FILE REPERENCE: P-LJ 3443
CURRENT APPLICATION NUMBER: US/09/258,754
CURRENT FILING DATE: 1999-02-26
FARLIER APPLICATION NUMBER: 09/042,107
BARLIER FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 452
SOFTWARR: Patentin Ver. 2.0
SEQ ID NOS: 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
           Sequence 3, Application US/09079432
; Patent No. 595572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pagualini, Ernata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; STREET: California
; COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER PRADABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: BARCHEN
SOFTWARE: PACENTIA Release #1.0, Version #1.25
SOFTWARE: PACENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,432
FILING DATE:
CLASSIFICATION NUMBER: US 08/520,535
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/520,535
FILING DATE: 28-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LA 1794
TELECOMMUNICATION INFORMATION:
TELEFRX: (619) 535-9001
TELEFRX: (619) 535-9001
TELEFRX: (619) 535-901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33, Application US/09258754 Patent No. 6174687 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.5
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CWDDGLMC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-258-754-33
US-09-079-432-3
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FEATURE:
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US-09-042-107-42
is Gaquence 42, Application US/09042107
is Batent No. 623287
is German. Information:
is APPLICANT: Ruoslahti, Erkki
is APPLICANT: Ruoslahti, Erkki
is APPLICANT: Pasqualini, Renata
i TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
iTITLE OF INVENTION: Tissues
is FILE REFRENCE: P-LJ 2892
is CURRENT APPLICATION NUMBER: US/09/042,107
is SUFFWARE: PAPPLICATION NUMBER: 1998-03-13
is NUMBER OF SEQ ID NOS: 436
is SEQ ID NO 42
i LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                       GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ruoslahti, Erkki

APPLICANT: Pasqualini, Remata

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION: Molecules that Home to Various Selected Organs or

TITLE OF INVENTION MOMBER: US/09/042,107

CURRENT APPLICATION NUMBER: US/09/042,107

CURRENT FILING DATE: 1998-03-13

SOFTWARE: PATENTIN VOS: 436

SOFTWARE: PATENTIN VOS: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-42
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US-09-042-107-214
; Sequence 214, Application US/09042107
; Patent No. 632287
; GENERAL INFORMATION:
                                                                                                             %3-09-042-107-33
; Sequence 33, Application US/09042107
; Patent No. 6232287
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%;
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Best Local Similarity 50.0
Matches 4; Conservative
                       1 CFKSTLLC 8
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1 CHEGYLTC 8
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Best Local Similarity
Matches 4; Congery
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## APPLICANT: Ruoslahti, Erkki
## APPLICANT: Ruoslahti, Erkki
## APPLICANT: Raoqualini, Renata
## TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
## TITLE OF INVENTION: Tissues
## FILE REPERRICE: P-LJ 2892
## CURRENT FILING DATE: P-LJ 2892
## CURRENT FILING DATE: 1998-03-13
## ANUMERS OF SEQ ID NOS: 436
## ANUMERS OF SECTION OF ARTIFICIAL SEQUENCE: Synthetic
## ORGANISM: Artificial Sequence
## ANUMERS OF SECTION OF ARTIFICIAL SEQUENCE: Synthetic
## OF ANUMERS OF SECTION OF ARTIFICIAL SEGUENCE
## ANUMERS
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2004, 12:07:41; Search time 20 Seconds (without alignments) 52.905 Million cell updates/sec

Title: US-09-761-636A-7

Ferfect score: 61 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapox 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1327

Minimum DB seq length: 0

Maximum DB seq length: 11
```

Post-processing: Minimum Match 10%

Maximum Match 100%
Listing first 45 summaries

Listing first 45 summaries

Listing first 45 summaries

1: pir: **
2: pir: **
3: pir: **
4: pir: **
4: pir: **
4: pir: **
6: the number of results predicted by chance to hav

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	E C	D57789	I65546	A60521	C39191	33008	C39111	PH0944	S21727	PH0929	T51049	750778	A00330	1 47013	262880	A61622	PH0926	A32195	ECLO2M	500616	B59272	PH1 5 R4	DNO042	DHOGAT	110000	2012/4	A35039	PC1316	308996	B49823	B44960	A33995
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о́н	24	36.1	32.8	31.1	29.5		27.9	27.9	27.9		26.2		26.2				٠		26.2		24.6					٠	٠	73.0	٠	23.0	23.0	23.0
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	Result No.		7	e	4	Ŋ	9	7	60	O)	10	11	12	13	1.	* 1	G .	16	17	18	19	20	. 21	22	23	200		7 6	56	27	28	29

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2 PL0184	2 A42057	2 A33180 2 B41983	2 A29477	2 152974	1 XAVI6B	2 JC1416	2 809138	2 B33995		2 PA0050		, 12	1 VACATES	Hancoo	2 S58244
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30	3.5	333	34	35	36	37	38	39	40	41	42	43	44	9.0	n r

ALIGNMENTS

RESULT 1

D57789 gallbladder stone matrix protein, 14.5K - human (fragment) C;Species: Home sapiens (man) C;Species: Bome sapiens (man) C;Date: 23-Reb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996 C;Accession: D57789 R;Binette, J.P.; Binette, M.B. submitted to the Protein Sequence Database, February 1996 A;Pescription: The proteins of gallbladder stones. A;Reference number: A57789 A;Reference number: A57789 A;Reference to the protein at the proteins of gallbladder stones. A;Reference to the protein by protein A;Residues: preliminary A;Melecule type: protein A;Residues: 1-11 cAIN>	Query Match 36.1%; Score 22; DB 2; Length 11; Best Local Similarity 66.7%; Pred, No. 8.2e+02; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 5 PLISVP 10 Db 1 PATSAP 6	RESULT 2 165546 MHC H2-L antigen - mouse (fragment) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Accession: 16546 R;Accession: 16546 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P. Cell 44, 261-272, 1986 A;Title: Detailed analysis of the mouse H-ZKD promoter: Enhancer-like sequences and the A;Reference number: 152778; MUID:8610620; PMID:3510743 A;Accession: 165546 A;Accession: 165546 A;Accession: humary; translated from GB/EMBL/DDBJ	Argonecuse type: Luka Argonecuses: 1-6 <res> Arcoss-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234 Query Match Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 9 VPC 11 Db 2 VPC 4</res>	
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RESULT 3 A60521 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

Mon Mar

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C,Accession: C33111
R;Varner, J.; Neame, P.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991
A;Title: A serum heterodimer from hagfish (Eptatretus stoutii) exhibits structural simi
A;Reference number: A39111; MUID:91156684; PMID:2000382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RiGold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg
A;Reference number: PHOB91; MUID:92078857; PMID:1836012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: $21727
R;Wei, M.L.; Cresswell, P.
Nature 356, 443-446, 1992
A;Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence-A;Reference number: $21727; WUID:92212461; PMID:1557127
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                                       Ig heavy chain C region - Pacific hagfish (fragment)
C;Species: Eptatretus stouti (Pacific hagfish)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.9%; Score 17; DB 2; Length 11; 37.5%; Pred. No. 6.2e+03; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                               27.9%; Score 17; DB 2; I
nlarity 80.0%; Pred. No. 5.6e+03;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Moleoule type: protein
Asseidues: 1-10 «VAR»
C;Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 37.5
Matches 3; Conservative
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Best Local Similarity
----a 3; Conserv?
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A;Molecule type: protein
A;Residues: 1-11 <WEI>
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Best Local Similarity
Matches 4; Conserv
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A;Molecule type: mRNA
A;Residues: 1-10 <GOL>
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NiAlternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Species: Liza ramada
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 235-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mus A;Reference number: A60521; MUID:90227907; PMID:2109669
A;Accession: A60521
A;Accession: A60521
A;Accession: A60521
C;Superfamily: glucan phosphorylase
C;Keywords: 1-5 - 80N>
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein 1 (Tetx 5' region) - Bacteroides fragilis
C;Species: Bacteroides fragilis
C;Species: Bacteroides fragilis
C;Jote: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 30-Sep-1993
C;Accession: C3191
R;Speer, B.S.; Bedzyk, L.; Salyers, A.A.
J; Bacteriol. 173, 176-183, 1991
J; Bacteriol. 173, 176-183, 1991
A;Reference that a novel tetracycline resistance gene found on two Bacteroides tra
A;Reference number: A39191; MUID:91100280; PMID:1846135
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C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: 633098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                     31.1%; Score 19; DB 2; Length 5; 100.0%; Pred. No. 2.8e+05; ative 0; Mismatches 0; Indels
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Pred. No. 2.8e+05;
0; Mismatches 2; Indels
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29.5%; Score 18; DB 2; I
Local Similarity 57.1%; Pred. No. 3.8e+03;
hes 4; Conservative 1; Mismatches 2;
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Best Local Similarity 100.0
Matches 4; Conservative
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A;Molecule type: protein
A;Residues: 1-8 <NIC>
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Matches
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vitellogenin, 190k chain - gypsy moth (fragment)
N;Contains: vitellin
C;Species: Lymantria dispar (gypsy moth)
C;Species: Lymantria dispar (gypsy moth)
C;Date: 21-Uul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C;Accession: A61622
C;Accession: A61622
Insect Biochem: Mol. Biol. 22, 605-611, 1992
A;Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantry
A; Reference number: A61622
                                                                                                                                                   R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0247
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                                        Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)
C;6pctes: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Aspergillus sp.
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S62880
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ERSB Lett. 382, 164-166, 1996
A;Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A;Reference number: S62880; MUID:96196586; PMID:8612742
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                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-9 < YZMA-
A; Residues: 1-9 < YZMA-
A; REsperimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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Best Local Similarity 50.0%,
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A,Status: preliminary
A,Molecule type: protein
C,Residues: 1-10 cHIR>
C,Reywords: egg yolk; hemolymph
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A;Molecule type: protein
A;Residues: 1-10 <STR>
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                     C; Species: Rattus norvegicus (Norway red.) - rat (Iragment)
C; Species: Rattus norvegicus (Norway red.)
C; Date: 09-0ct-1992 #sequence_revision 09-0ct-1992 #text_change 30-May-1997
C; Accession: PH0929
R; Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A; Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi A; Accession: PH0929
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A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A;Reference number: A60356; MUID:90216080; PMID:2323853
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C;Species: Oncorbynchus mykiss (rainbow trout)
C;Species: J3-8ep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss)
A;Reference number: I51049; MUID:95324545; PMID:7601121
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A;Molecule type: DNA
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328
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C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60356
R;Shiraishi, Y.
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T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
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                                                                                                                                                                                                                                                                                                                       A;Experimental source: concanavalin A-activated lymphoblast C;Keywords: T-cell receptor
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A;Molecule type: protein
A;Residues: 1-9 <SHI>
C;Keywords: glycoprotein
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Matches 2: Conserv
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A; Residues: 1-11 <GOL>
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PH0926
T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: PH0926
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Residues: 1-10 cGOL
A;Residues: 1-10 cGOL
A;Residues: 1-10 cGOL
A;Rolecule type: mRNA
A;Residues: ranslated the codon AGA for residue 4 as Thr
C;Keywords: T-cell receptor
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26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                  141681 segs, 52070155 residues
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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61
1 CISVPLTSVPC 11
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries SwissProt_42:* Database :

Minimum DB seq length: 0 Maximum DB seq length: 11

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P82654 hoplobatrac P82654 hoplobatrac P82651 hoplobatrac P58785 conus purpu P29177 bos taurus P30090 homo sapien P41488 locusta mig P14595 tabanus atr P64549 periplaneta P30096 homo sapien P16319 locusta mig P64549 periplaneta P30096 homo sapien P16319 locusta mig P52825 azotobacter P01022 bothrops in P1385 carausius m P14596 tabanus atr P30424 bothrops in P30424 bothrops in P30424 bothrops in P30424 bothrops in P30425 bothrops in P30422 bothrops in P30422 bothrops in P30432 bothrops in P30435 uncorhymedus P81135 mycobacteri P8135 gachymedus P8115 mycobacteri P81455 pachymedus P8110 fusarium so P81780 herpes simp P83320 penaeus mon
SUMMARIES	TIN4 HOPTI TIN1—HOPTI CONZ—CONPU WEAT BOVIN UPA4—HUMAN CXII_COMMR LIPEZ_LOCMI HPEZ_PERAM UPAA—HUMAN DNFI_LOCMI YEER AZOVI BPPZ_PERAM HTFZ_CARU BPPZ_BOTIN COXIZ_STEEP BRAZ_STEAS OXIZ_STEEP BRAZ_STEAS ALLE_CYDPO FURSZ_FURSZ BYCTU ANGLE ARVZB RAZ_FURSZ BYCTU ANGLE ARVZB FURSZ BYCT
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Score	10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Result No.	11111111111111111111111111111111111111

RESULT 2

IN1 HOPET

IN HOPET

AC P02651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 43, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DC Edukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; OC Hoplobatrachua

OX NCBL TaxID=103373;
RN [1]
RP SEQUENCE; FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;

[1] SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS. TISSUE=Skin secretion;

9 1 FLA2_TREHY 9 1 OXXT BUFRE 9 1 SAP_STOVA 10 1 TALZ_LOCMI 10 1 TALZ_LOCMI 11 1 T2P1_ROCVU 6 1 VPA8_HUMAN 7 1 CARP_WITED 7 1 CARP_WITED 7 1 CARP_WITED 8 1 PPK3_PERAM 8 1 PPK3_PERAM 9 1 COXE_THUOB 9 1 COXE_THUOB 9 1 FAR9_ASCSU	T.1 TIN4 HOPTI TIN4 HOPTI TIN4 HOPTI TIN5 HOPTI TIN6 HOPTI T	JOHN TOTAL T
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methylguanine-DNA methyltransferase) (Fragment).
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01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
STRAIN-Clipperton Island; TISSUR-Venom;
MEDLINE-99388839; PubMed=10461743;
Jacobsen R.B., Jimenez B.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                   Gaps
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           Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
Devi A.S., Nagaraj R., Sitaram N.;
"Tigerinins: novel antimicrobial peptides from the Indian frog Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                olivera B.M.;

"A novel D-leucine-containing Conus peptide: diverse conformational dynamics in the contryphan family.";

J. Pept. Res. 54:33-99(1999).

- SUBCELLULAR LOCATION: Secreted.

- TISSUE SPECIFICIE: Expressed by the venom duct.

- MASS SPECIFICM: Expressed by the venom duct.

- MASS SPECIFICMENTY: MAR-888 4; METHOD=LSIMS.

- SMILARITY: Belongs to the contryphan family.

DISULPID.

DISULPID.
                                                    J. Biol. Chem. 276:2701-2707 (2001).
-!- FUNCTION: Antibacterial activity against B.subtilis, B.coli, S.aureus, M.luteus, P.putida and S.cerevisiae.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUB SPECTROMPTS Shin.
-!- TISSUB SPECTROMERY: MM=1342; METHOD=MALDI.
--- MASS SPECTROMERY: MM=1342; METHOD=MALDI.
--- Amphibian defense peptide; Antibiotic; Funglcide; Amidation.
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0
                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbecconcha, Hypsogastropoda,
Neogastropoda, Concidea, Conidae, Conus.
VCBI_TaxID=41690;
                                                                                                                                                                                        Score 19; DB 1; Length 11;
Pred. No. 9.7e+02;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.5%; Score 18; DB 1; Length 8; 40.0%; Pred. No. 1.46+05; ive 2; Mismatches 1; Indels
                                                                                                                                                      AMIDATION.
A2087DC960476056 CRC64;

        MOD_RES
        4
        4
        D-LEUCINE.

        SEQUENCE
        8 AA;
        890 MW;
        75A367672732CEB8 CRC64;

                                                                                                                                                                                                                                                                                                                                               (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                          8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens (Purple cone)
                                                                                                                                                      MOD RES 11 11 SEQUENCE 11 AA; 1344 MW;
                                                                                                                                                                                          31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Conservative
                                                                                                                                                                                                                  2; Conservative
                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                       Query Match
Best Local Similarity
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CTMIPI 7
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CWLLP 6
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28-FEB-2003 (
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ID MGMT_BOVIN
AC P29177;
                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
                                              tigerina.";
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Matches
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Nucleic Acids Res. 18:17-21(1990).
--- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the 0-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is ireversibly inactivated.
--- CATALYTIC ACTIVITY: DNA (containing 6-0-methylguanine) +
[protein]-L-cysteine = DNA (without 6-0-methylguanine) + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-methyl-i-cysteine.
-!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLITRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
InterPro; IPR001497; Methyltransf_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                 MEDLINE=90174912; PubMed=2308822;
Rydberg B., Hall J., Karran P.;
"Active site amino acid sequence of the bovine O6-methylguanine-DNA
methyltranaferase."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Plasma protein map: an update by microsequencing.";

Blectrophoresis 13:707-714(1992).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 4.8, its MW is: 40.5 kDa.
-!- MISCELLANEOUS: This spot is on a position thought to be that of Zn-alpha-2 glycoprotein, but it does not correspond to that
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalía; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanches J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.7%; Score 17.5; DB 1; Length 9; 37.5%; Pred. No. 1.4e+05; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 10 10
10 AA; 1067 MW; 269492EB05A1A457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA; 967 MW; 325171A720476047 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Conservative
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Bos taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                              NCBI_TaxID=9913;
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Gaps

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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
Tabanus.
family.";
Comp. Biochem. Physiol. 106C:103-109(1993).
-!- FUNCTION; Mediates visceral muscle contractile activity (myotropic
                                      01-JAN-1990 (Rel. 13, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IFR002047; AKH.
PROSITE; PS00256, AKH; 1.
Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
MOD RES 8 AMIDATION.
MOD_RES 8 AMIDATION.
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                                                                                                                                                                                                                                                                                                Match Local Similarity 100.0%; Pred. No. 4.7e+03; Local Similarity 100.0%; Pred. No. 4.7e+03; Local Similarity 0; Mismatches 0; Indels les
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA; 949 MW; 86786771A9D1A736 CRC64;
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60.0%; Pred. No. 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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13-AUG-1987 (Rel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabanus atratus (Horse fly).
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Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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HTF2 PERAM
ID HTF2 PI
                                                                                                                                                                                                                                                                                                                   Query Match
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     S FF S BRCCCC RF S S FF S S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     venon of Conus marmoreus.";
yenon of Conus marmoreus.";
J. Biol. Chem. 275:39516-39522(2000).

-- FUNCTION: Inhibits the neuronal noradrenaline transporter.
-- SUBCELLUIAR LOCATION: Secreted.
--- IISSUE SPECIFICITY: Expressed by the venom duct.
--- RISSUE SPECIFICITY: Expressed by The venom duct.
--- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
Neurotoxin; Toxin; Hydroxylation.
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Venom;
MEDLINE=20564325; PubMed=10988292;
Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha, Acridoidea, Acrididae, Oedipodinae, Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apogastropoda; Caenogastropoda; Sorbecconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=42752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.2%; Score 16; DB 1; Length 11; 100.0%; Pred. No. 3.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
           Score 17; DB 1; Length 10; Pred. No. 2e+03;
                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 10 HYDROXYLATION.
11 AA; 1226 MW; 277AAC60B7232B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
1coustapyrokinin 2 (IOM-PK-2) (FXPRL-anide).
1cousta migratoria (Migratory locust)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA.
                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Lambda-conotoxin CMrVIA.
                                                                                                                                                                                                                                                                                                           11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. No. 3.4 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conus marmoreus (Marble cone).
                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
28-FEB-2003 (Rel. 41, Last ann
                      27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Conservative
  Query Match
Best Local Similarity 80.v.
                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seow K.T., Bay B.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                            4 VPLTS 8
                                                                                                                                                                         2 VPNTS 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
LPK2 LOCMI
ID LPK2 LOCMI
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PIK; A29477; A29477.
Interpro; IPROG981; Neurhyp_horm.
Pfem; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone; Neuropeptide; Amidation.
DISULFID 1 6 IN F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 23.0%;
Similarity 57.1%;
4; Conservative 0
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                                      STANDARD;
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                                                                                                                                                                       Homo sapiens (Human)
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Best Local Similarity
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                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                 01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCAL
                                        UPAA HUMAN
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DNF1 LOCMI
           UPAA HUMAN
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WEDLINE-90253659; PubMed-2340112;

A Gaede G., Rinehart K.L. Jr.;

Gaede G., Rinehart K.L. Jr.;

A Gaede G., Rinehart K.L. Jr.;

The corpora cardiaca of the cockroaches Leucophaea maderae,

the corpora cardiaca of the cockroaches Leucophaea maderae,

Toromhadorhina portentosa, Blattella gemanica and Blatta orientalis

Toromhadorhina portentosa, Blattella gemanica and Blatta orientalis

Toromhadorhina portentosa, Blattala assigned by tandem fast

and of the stick insect Extatosema tiaratum assigned by tandem fast

to combardorhina portenenty.";

Blot. Chem. HOppe-Sevier 371:345-354(1990).

Collevate the level of trehalose in the hemolymph (trehalose is the major carbohydrate in the hemolymph of insects).

Collevate the level of the AKH / HRTH / RPCH family.

PIR: B49802; B49803.

PIR: S08995; S08996.

PIR: S08995; S08996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-P. americana;
MBDLINE=84298179; PubMed=6591205;
Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
Miller C.A., Schooley D.A.;
"Isolation and primary structure of two peptides with
cardinaceleratory and hyperglycemic activity from the corpora
cardinaca of Periplaneta americana.";
Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-1. decemlineata; TISSUB-Corpora cardiaca;
MEDLINE-90160053; PubMed-2576128;
Gaede G., Kellner R.;
"The metabolic neuropeptides of the corpus cardiacum from the potato
beetle and the American cockroach are identical.";
Peptides 10:1287-1289(1989).
01-FEB-1994 (Rel. 28, Last sequence update)
110-OCT-2003 (Rel. 42, Last annotation update)
Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
(PeA-CAH-II) (LeD-CC-II) (Hypertrehalosaemic neuropeptide II).
                                                                                                                                                                                                                                                                                                                                                                                "Structures of two cockroach neuropeptides assigned by fast atom bombardment mass spectrometry.";
Biochem. Biophys. Res. Commun. 124:350-358(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                               SPECIES=P.americana;
BEDLINES-S046530; PubMed=6548628;
Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
Rinehart K.L. Jr.;
                                                                                                                                                      Enkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
NCBI_TaxID=6978, 7539, 6976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002047; AKH.
PROSITE; PS00255; AKH; 1.
Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 14; DB 1; Length 8; Pred. No. 1.4e+05; 0; Mismatches 2; Indels
                                                                                        Periplaneta americana (American cockroach),
Leptinotarsa decemlineata (Colorado potato beetle), and
Blatta orientalis (Oriental cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
86745771A9D1A736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1006 MW;
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Best Local Similarity
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SEQUENCE.

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Matches

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"Identification of an arginine vasopressin-like diuretic hormone from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 7, its MW is: 12 kDa.
                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IN F2).
(IN F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Plasma;
MEDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
12-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Suboesophageal ganglion, and Thoracic ganglion; MEDLINE-88077077; PubMed=5689410; Proux J. P., Miller C. A., Li J. P., Carney R.L., Girardie A., Delaage M., Schooley D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 14; DB 1; Length 8; Pred. No. 1.4e+05; 0; Mismatches 3; Indels
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INTERCHAIN (WITH C-6) (:
INTERCHAIN (WITH C-1) (:
AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 149:180-186 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F -> P.
/FTId=VAR_000004.
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01-AUG-1990 (Rel. 15, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Locupressin (Diuretic neuropeptide F1/F2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA.
8 AA.
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DISULFID
MOD RES
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NCBI TaxID=7022, 7024;
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Best Local Similarity
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HTF2_CARMO
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    STEEN CCCCRETER SO
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01-FBE-1994 (Rel. 28, Last sequence update)
428-FBE-2003 (Rel. 41, Last amnotation update)
Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bothrops jararaca (Jararaca).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Venom;
MEDLINE=72118526; PubMed=4334402;
Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,
                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Azotobacter.
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                                    Score 14; DB 1; Length 9; Pred. No. 1.4e+05; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.0%; Score 14; DB 1; Length 9; 75.0%; Pred. No. 1.4e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Unification of the ferritin family of proteins.";
Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
56EB176EB451A057 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA; 947 MW; DF98B5A1B417776D CRC64;
                                                                                                                                                                                                                                                                                                    01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-COT-2001 (Rel. 40, Last annotation update)
Hypothetical protein in bfr 3/region (Fragment).
                                                                                                                                                                                                                                                                9 AA.
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MEDLINE=92196129; PubMed=1549605;
                                      23.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M83692; AAA22122.1; -.
                     Query Match
Best Local Similarity 40.0%,
    976 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 75.0
nes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         Azotobacter vinelandii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B41983; B41983.
Hypothetical protein.
                                                                                                                      6 LTSVP 10
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                                                                                                                                                  :|: |
3 ITNCP 7
    9 AA;
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                                                                                                                                                                                                                        RESULT 12
YBFR_AZOVI
ID_YBFR_AZOVI
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    SEQUENCE
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P01022;
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MEDIJINE=90253659; PubMed=2340112;
Gaede G., Rinehart K.L. Jr.;
"Primary structures of hypertrehalosaemic neuropeptides isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES—C.morosus; TISSURE-Corpora cardiaca; MEDLINE-93129118; PubMed=1482345; Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.; Atryptophan-substituted member of the AKK/RPCH family isolated from a stick insect corpus cardiacum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a stick insect corpus cardiacum.";
Biochem. Biophys. Res. Commun. 189:1303-1309 (1992).
-!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
elevate the level of trehalose in the hemolymph (trehalose is the
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
the corpora cardiaca of the cockroaches Leucophaea maderae,
Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
and of the stick insect Extatosoma tiaratum assigned by tandem fast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (Rel. 11, Created)
01-FRB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypertrehalosemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic neuropeptide II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extatosoma tiaratum (Stick insect).
Sukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Phasmatodea, Euphasmida, Phasmatoidea,
Heteromemidae, Carausius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum of the Indian stick insect, Carausius morosus, determined by fast atom bombardment mass spectrometry."; Biol. Chem. Hoppe-Seyler 368:67-75(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                              Score 14; DB 1; Length 10; Pred. No. 7.1e+03; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major carbohydrate in the hemolymph of insects).
-!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW-1308.61; METHOD-FAB.
-!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
PIR; 509138; 509138.
                                                                                                                                                                                                                                                                                                     10 AA; 1232 MW; 30C53546C7741773 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carausius morosus (Indian stick insect), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atom bombardment mass spectrometry.";
Biol. Chem. Hoppe-Seyler 371:345-354(1990).
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33.3%;
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RESURE—Corpora cardiaca;

RESURE—Corpora cardiaca;

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RESURE—Corpora cardiaca;

RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,

RA Joffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,

RA Joffe H., Raina A.K., Riley S.D.K.;

RA Primary Structure of two neuropeptide hormones with adipokinetic and

RT "Primary Structure of two neuropeptide hormones with adipokinetic and

RT "Primary Structure of two neuropeptide hormones with adipokinetic and

RT "Primary Structure of two neuropeptides that

FILES (Diptera).",

RT Trehalosemic factors are neuropeptides that

elevate the level of trehalose in the hemolymph (trehalose is the

elevate the level of trehalose in the hemolymph (trehalose is the

elevate the level of trehalose in the hemolymph (trehalose is the

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relevate the level of trehalose in the hemolymph (trehalose is the

relevate the level of trehalose in the hemolymph of insects).

InterPro; IPRO02047, AKH.

RESUBLIGHAN SCOZES, AKH.

RENOSITE, PSO025S, AKH.

RENOSITE, PS
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01-FBH-1994 (Rel. 28, Last sequence update).
10-OCT-2003 (Rel. 42, Last annotation update)
Hypertrahalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II)
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
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InterPro; IPR002047; AXH.
PR05TTE; PS00256, AXH; 1.
Neuropepide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
MOD_RES 1 1 1 PYRROLIDONE CARBOXYLIC ACID.
CARBOGYD 8 R C-LINKED (MAN) (FR0BABLB).
CARBOOTD 10 ANIDATION.
SEQÜENCE 10 AA; 1164 MM; 9B9036745771A9D1 CRC64;
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Pred. No. 7.1e+03;
0; Mismatches 2; Indels
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Pred. No. 7.1e+03;
0; Mismatches 2; Indels
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Best Local Similarity 60.03
Matches 3; Conservative
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P14596;
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HTF_TABAT
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q9tqs0 bos taurus	Q8gmm5 acinetobact	Q85598 moloney mur	Q85563 moloney mur	Q85619 moloney mur	Q56140 streptococc	Q9tkf7 agonis gran	Q9tkf9 melaleuca v	Q9tkg2 callistemon	Q9tkfl homalosperm	Q9tkf8 tristaniops	Q9tkf4 angasomyrtu	Q9tkf3 asteromyrtu	Q9tke0 neofabricia	Q9tkf0 kunzea ambi	Q9tkf6 agonis obtu
	ΙΩ	09T0S0	OBGMM5	085598	085563	085619	056140	Q9TKF7	Q9TKF9	Q9TKG2	Q9TKF1	Q9TKF8	Q9TKF4	Q9TKF3	Q9TKE0	Q9TKF0	Q9TKF6
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Query Match
34.4%; Score 21; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.6e+03;
Matches 4; Conservative 2; Mismatches 1; Indels

3 SVPLTSV 9 : | | : | | 3 AVPVVSV 9

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OBGMMS PRELIMINARY; PRT; QBGMMS; (TrEMBLrel. 23, Created)

RESULT 2 QBGMM5 ID QBGMMA AC QBGMMACDT 01-ME

Ogthm7 leptospermu Ogtke2 leptospermu Ogtke3 leptospermu Ogtke3 leptospermu Ogtke7 kunzea pulc Ogtke6 leptospermu Ogtke6 leptospermu Ogtke8 leptospermu Ogtke1 neofabricia Ogtke4 leptospermu Ogtke7 lophostemon P83092 spinacia ol Ogtx10 lilium long Ogty38 homo sapien Ogty38 homo sapien		pdate) update)	Craniata; Vertebrata; Buteleostomi; actyla; Ruminantia; Pecora; Bovoidea; ., Klungland H.; c-kit gene."; MBL/GenBank/DDBJ databases
Q9THM7 Q9TKE2 Q9TKE3 Q9TKE3 Q9TKE7 Q9TKE6 Q9TKE6 Q9TKE8 Q9TKE4 Q9TKE4 Q9TKE4 Q9TKE4 Q9TKE7 Q9TKE7 Q9TKE7 Q9TKE7 Q9TKE7 Q9TKE7	000 0000	ALIGNMENTS PRT; 11 AA. Created) Last sequence update) Last annotation update)	ு ஜ ஜெய்ட்
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	17. 17. 17. 17. 17. 17. 17. 17. 17. 17.	4 FFXE	Eukaryota, Metazoa; Ch Mammalia; Eutheria; Ce Mammalia; Eutheria; Ce Bovidae; Bovinae; Bos. (1) EuxID=9913; (1) ExQUENCE FROM N.A. Olsen H.G., Vage D.I., "A polymorphism in the Submitted (JUN-1999) V. EMBL; AJZ43424; CAB607 EMBL; AJZ43424; CAB607 EMBL; AJZ43424; CAB607 EMBL; AJZ43426; CAB607 EMBL; AJZ43426; CAB607 EMBL; AJZ43426; CAB607 NON TER 11 SEQÜENCE 11 AA; 112
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Donoghue D.U., Hunter T.,
"A generalized method of subcloning DNA fragments by restriction site
reconstruction: Application to sequencing the amino-terminal region of
the transforming gene of Gazdar murine sarcoma virus.";
Nucleic Acids Res. 10:2549-2564(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-83164305; PubMed=6300424;
Donoglube D.J., Hunter T.;
"Recombination junctions of variants of Moloney murine sarcom virus:
"Recombination and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).
BMBL; K03108; AAA46494.1; -.
NON TER 10 10
SEQÜENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;
                                                                                                                                                                                                                                                                                                                                         Donoghue D.J., Hunter T.;
"Recombination junctions of variants of Moloney murine sarcom virus:
Generation and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).
EMBL; K03105; AA46491.1; -.
NON TER
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DOC-2001 (TrEMBLrel. 19, Last annotation update)
Moloney murine sarcoma virus (Strain m1) env/mos 5' junction
(Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.8%; Score 20; DB 15; Length 10; 75.0%; Pred. No. 5e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moloney murine leukemia virus.
Vinuses; Retroid viruses; Retroviridae; Gammaretrovirus.
NCBI_TaxID=11801;
                                                                                                                               Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
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                          Q85563 PRELIMINARY; PRT; 10 AA.
Q85563; Q85563; Q85060; GTEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                     Env-mos fusion protein (Fragment).
Moloney murine leukemia virus.
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MEDLINE=83164305; PubMed=6300424;
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Q56140
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Q85619
RESULT 4
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MEDLINE=83164305; PubMed=6300424;
MEDLINE=8316405; PubMed=6300424;
Donoghue D.J., Hunter T.;
Recombination junctions of variants of Moloney murine sarcom virus:
Recombination junctions of a mammalian transforming gene.";
Generation and divergence of a mammalian transforming gene.";
J. Virol. 45:607-617(1983).
BMB: K03106; AAA46492.1; -.
NON TER
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BW3; PLASMID-PKLH207;
Kholodii G.Y., Mindlin S.Z., Gorlenko Z.M., Yurieva O.V.,
Kholodii G.Y., Minkiforov V.G.;
"A young family of transposable adaptive DNA segments identified in the Acinetobacter genus.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ250234, ZGA9784.1; --
EMBL; AJ486885; CAD31078.1; --
GQ; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                          STRAIN=BW3; PLASMID=pKLH207;
Kholodi G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
Nikiforov V., Warieva transposons and possible mechanisms of their
"pKiH2-like aberrant transposons and possible mechanisms of their
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                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Moloney murine sarcoma virus (Strain HTI) env/mos 5' junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.8%; Score 20; DB 15; Length 10; 75.0%; Pred. No. 5e+03; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.8%; Score 20; DB 2; Length 8; 80.0%; Pred. No. 1e+06; tive 0; Mismatches 1; Indels
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Moloney murine leukemia virus.
Viruses, Retroid Viruses; Retroviridae; Gammaretrovirus.
                                                                                                                                                                                                                                                    Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;
    Last sequence update)
Last annotation update)
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SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;
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   01-MAR-2003 (TrEMBLrel. 23, 01-JUN-2003 (TrEMBLrel. 24, Transposase (Fragment).
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                                                                   Acinetobacter Bp. BW3.
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Best Local Similarity
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Best Local Similarity
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                                                                                 Plasmid pKLH207
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Q85598
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SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 480-0 (2000).
EMBL; AR184666; AAPO386.1; -.
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                     SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
Wolecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
EMBL, Bot. 48:0-0(2000).
EMBL, AR184670; AAR03640.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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                                                               Juracycta; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Melaleuca.
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ArpB (Fragment).
ATPB.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Query Match
Best Local Similarity 66./",
Asa 4; Conservative
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                                       Melaleuca viridiflora.
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                                                                                                           NCBI_TaxID=106062;
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                (Fragment)
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
EMBL. J. Bot. 48:0-0(2000).
EMBL. AFP1846715, AAF03485.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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Chloroplast.

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
Myttales, Myttaceae, Agonis.

NCBL_TaxID=106028,
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                 Streptococcus thermophilus.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                           01.NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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FEMS Microbiol. Lett. 122:85-90(1994).
EMBL, X78210; CAA55045.1; -.
B 8 8 8 SEQÜENCE 8 AA, 846 MM; ED086772D5B045B6 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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  8 AA.
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MEDLINE=95047254; PubMed=7958782;
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                                                                        STP6 protein (Fragment).
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                           NCBI_TaxID=1308;
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SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
Nofectiar Mystematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:621-628(2000).
                                                                                          SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
O'Brien M.M., Quinn C.J., Wilson P.G.;
Wholecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48-0-03(2000).
EMBL; AP184678; AAR0348.1; -.
GO; GO:0009507; C:chloroplast; IEA.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Myrtaceae; Asteromyrtus.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF184679; AAF03849.2; -..
GO; GO:0009507; C:chloroplast; IEA.
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
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66.7%; Pred. No. 7.6e+03;
tive 0; Mismatches 2;
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                              Myrtales; Myrtaceae; Angasomyrtus.
NCBI TaxID=106032;
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Matches 4; Conservative
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66.7%;
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SEQUENCE 10 AA; 1172 MW;
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Best Local Similarity 66.7-
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SEQUENCE FROM N.A.
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O'Brien M.M., Quinn C.J., Wilson P.G.;
O'Brien M.M., Quinn C.J., Wilson P.G.;
Wholeoular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0 (2000).
EMBL; AF184672; AAF03842.1; -.
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                          O'Brien M.M., Quinn C.J., Wilson P.G.;
"Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0(2000).
EMBL; AF184682; AAF03852.1; -.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Myrtacee; Tristaniopsis.
                                                  Eukaryoza, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Homalospermum.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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Pred. No. 7.6e+03;
0; Mismatches 2; Indels
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01-MAY-2000 (TrEMBirel. 13, Last sequence update)
01-JUN-2003 (TrEMBirel. 24, Last annotation update)
AtpB (Fragment)
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10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
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01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-JUN-2003 (TEMBLrel. 24, Last annotation update)
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66.7%;
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Chloroplast.
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Best Local Similarity
Matches 4; Conserva'
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                      Homalospermum firmum.
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                                                                                                                         NCBI_TaxID=106039;
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ATPB.
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O'Brien M.M., Quinn C.J., Wilson P.G.;

O'Brien M.M., Quinn C.J., Wilson P.G.;

Wolecular Systematics of the Leptospermum Suballiance (Myrtaceae).";

Aust. J. Bot. 48:0-0 (2000).

EMBL; AF184683; AAF03853.1; -.

GO; GO:0009507; C:chloroplast; IEA.

Chloroplast. 10

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SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;
                                                                                                                                              SEQUENCE FROM N.A.
O'Brien M.M., Quinn C.J., Wilson P.G.;
O'Brien M.M., Quinn C.J., Wilson P.G.;
Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
Aust. J. Bot. 48:0-0(2000).
BMBL, AR184700; AAP03869.1; -.
GO, GO:0009507; C:chloroplast; IEA.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota, Varidiplantae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Kunzea.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Myrtales; Myrtaceae; Neofabricia.
NCB_TAXID=106065;
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Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels
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31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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AtpB (Fragment).
ATPB.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

SUMMARIES

	Description						VEGF		•		CA12	SH2	Aaw12615 SH2 bindi	Abp47579 N. mening	ż	Aar77368 SH3 bindi		Aay41619 Mammalian		Aay26265 IBolated		Human	Abg64264 Human alb	Aar96138 Protease		Aaw46562 Peptide b
COLUMNICATION	CI.	AAU04526	AAU04542	AAU04545	AAU04543	AAU04544	AAU04532	AAU04533	AAU04529	AAR58418	AAE34703	AAW12561	AAW12615	ABP47579	ABP47580	AAR77368	ABP47596	AAY41619	AAR58417	AAY26265	ABR56927	AAG73418	ABG64264	AAR96138	AAW82212	AAW46562
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ALIGNMENTS

Human, VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. .11 /note= "This bond cyclises the peptide" Cendron A; Location/Qualifiers 1..11 Stacker S, AAU04526 standard; peptide; 11 AA. VEGF based monocyclic peptide 3. (LUDW-) LUDWIG INST CANCER RES. 18-JAN-2001; 2001WO-US001533. 18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. (first entry) Achen MG, Hughes RA, Key Disulfide-bond WO200152875-A1. 26-JUL-2001. 26-SEP-2001 Synthetic AAU04526; RESULT 1 AAU04526

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VBGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabeta carbon separation distances on opposite antiparallel strands of a

Example 25; Page 47; 102pp; English.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic conversation are used to interfere with angiogenesis, co cyclisation are used to interfere with angiogenesis, condition is diabetic retinopathy, psoriasis, arthropathy. The condition is diabetic retinopathy, psoriasis, arthropathy, recentered by angiogenesis, neovascularisation or lymphangiogenesis. The condition, is diabetic retinopathy, psoriasis, arthropathy, creceptovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive crauma, substance-induced neovascular sequelae, or chronic liver sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic curbant at least one biological activity induced by VEGF-C or -D and care also used in combination with an anti-inflammatory agent, to treat a structure. The contractory agent, to treat a structure contractory and arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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diabetes induced neovascular sequelae, rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic.
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100.0%; Pred. No. 0.0016;
iive 0; Mismatches 0; Indels
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16-MAY-2000; 2000US-0204590P.
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HARAMA X B X X B X X B B X B B X B X X B B X X B X X B B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human concern of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a cyclising the peptides of meric bicyclic peptides no especially oxidishing the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior peptides) and a cyclic peptide with at least one amino acid deleted prior comparaterisation or lymphanglogenesis, na mammal with a condition characterised by anglogenesis, neovascularisation or lymphanglogenesis, neovascularisation or lymphanglogenesis, neovascularisation or lymphanglogenesis. The manual was diabetic retinopathy, psoriasis, arthropathy, hemangloma, vascularised malignant or benign tumour, post recovery cerebrovascular accident, post-mignopathy restenosis, head, heat or cold crauma, substance-induced neovascularisation of the liver, excessive trauma, substance-induced neovascularisation of the liver, excessive corporate anglogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, nypertension induced neovascular sequelae, or chronic liver corporation in peripheral limbs or in lungs, peritoneal cavity, pleura, accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic current a least one biological activity induced by VEGF. Or -D and cremonic inflammation, especially rheumatoid arthritis, psoriasis and cremonic arthritis and crivity induced by VEGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, VEGF; vascular endothelial growth factor; angiogenesis;
neovascularisation; lymphangiogenesis, psoriasis, tumour;
diabetes induced neovascular sequelae; rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 4; Length 11;
Pred. No. 0.0034;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "This bond cyclises the peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU04545 standard; peptide; 11 AA.
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16-MAY-2000; 2000US-0204590P.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CISVPLTSVPC 11
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1 CLSVPLTSVPC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11 AA;
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AAU04543;
                                 Query Match
                                  Matches
                                        RESULT 4
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human whose 3-dimensional structure is modelled on the expose loop of human C whose 3-dimensional structure is modelled on the expose loop of human composed on the control of producing a monomeric monocyclic peptide by a measuring beta-character of producing a monomeric monocyclic peptide by a measuring beta-character of peptide by oxidising the cysteine residues. The monocyclic peptides in meric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior complication are used to interfere with anglogenesis.

The conditionistion or lymphanjogenesis in a mammal with a condition characterised by anglogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy peoriasis arthropathy.

The mangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angloplasty restenosis, head, heat or cold formula. The condition is the liver, excessive commune.
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                                                                                                                                                                                                                             Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hormone related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
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diabetes induced neovascular sequelae, rheumatoid arthritis,
diabetic retinopathy; chronic inflammation, cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 4; Length 11; Pred. No. 0.0072; 2; Mismatches 0; Indels
                                                                               Cendron A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04543 standard; peptide; 11 AA.
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                                                                               Stacker S,
(LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.4%;
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                                                                                    Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diabetic retinopathy
                                                                                                                                                               WPI; 2001-442248/47.
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The sequence represents a monomeric monocyclic peptide or the invenition, whose 3-dimensional structure is modelled on the expose loop of human veger (vascular endochelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-expect of producing a monomeric monocyclic peptide by a measuring beta-expect of peptides of producing a monomeric monocyclic peptide such strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic certovatilarisation or lymphangiogenesis, neovascularisation or lymphangiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive corporation. The peptides are also used to modulate vascular permeability corporation in peripheral limbs or in lungs, peritoneal cavity, pleura, accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, corporation in peripheral limbs or in lungs, peritoneal cavity, pleura, corporation in peripheral limbs or in lungs, peritoneal cavity, pleura, corporation in peripheral limbs or in lungs, peritoneal cavity, pleura, corporation inflamention, especially rheumatory agent, to treat a condition especially rheumatory agent, to treat a corporation especially rheumatory agent, to treat a corporation especially rheumatoid arthritis, psoriasis and acciding archivors.
                                                                                                                                                                                                                                                                                                                       Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents a monomeric monocyclic peptide of the invention,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.5%; Score 54; DB 4; Length 11; 72.7%; Pred, No. 0.023;
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                                                                                                                                                                                                                                         Cendron A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04544 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                           Stacker S,
                                                                                                                                                                                               (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                               18-JAN-2000; 2000US-0176293P.
                                                                                                                                                    16-MAY-2000; 2000US-0204590P.
                                                                                    18-JAN-2001; 2001WO-US001533.
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                                                                                                                                                                                                                                           Hughes RA,
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Best Local Similarity
                                                                                                                                                                                                                                                                                        WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11 AA;
WO200152875-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2001
                                          26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04544;
                                                                                                                                                                                                                                              Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU04544
  2 X E X E X E X E
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1. .11 /note= "This bond cyclises the peptide"

Disulfide-bond

AAU04532;

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The sequence represents a monomeric monocyclic peptide of the invention, compose 3-dimensional structure is modelled on the expose loop of human vector whose 3-dimensional structure is modelled on the expose loop of human vector period a monomeric monocyclic peptide by a measuring beta-competed of producing a monomeric monocyclic peptide by a measuring beta-competed loop fragment from an exposed loop of a growth factor protein and peptides limeric bicyclic peptides with a least one amino acid deleted prior cyclising the peptides with a least one amino acid deleted prior peptides) and a cyclic peptide with at least one amino acid deleted prior cyclising the peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides with at least one amino acid deleted prior correcterised by angiogenesis in a mammal with a condition characterised by angiogenesis in a mammal with a condition of abbetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive cerebrovascular angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver competides are also used to monditate wacular permeability accumulation in peripheral limbs or in lungs, peritomeal cavity, pleura, cor brain. The peptides are used to image blood vessels and lymphatic cor with at least one biological activity induced by vEGF, vEGF or -D and are also used in combination with an anti-inflammatory agent, to treat a correct or perior certification with an anti-inflammatory agent, to treat a disparic retinance in a mammal sequelae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
diabetes induced neovascular sequelae, rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                            /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 25; Page 47; 102pp; English.
                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                             (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                           18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                               18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-442248/47.
                                                                                                                                            Disulfide-bond
                                                                                                                                                                                                             WO200152875-A1
                                                                                                                                                                                                                                                         26-JUL-2001.
                                                                               Synthetic.
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Cendron A;

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;
0
                                       Gaps
                                       ô
                 Score 52; DB 4; Length 11; Pred. No. 0.049;
                                       0; Indels
                                         3; Mismatches
                    85.2%;
72.7%;
                                          8; Conservative
                                                                              |||:|::||||
CISLPISSVPC 11
                                                                1 CISVPLTSVPC 11
                             Local Similarity
Sequence 11 AA;
                       Query Match
                                            Matches
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ï

Gaps

;

Score 45.5; DB 4; Length 10; Pred. No. 0.52; 0; Mismatches 0; Indels

74.6%; 90.9%;

10; Conservative

Best_Local Similarity Matches 10; Conserv

AAU04532 standard; peptide; 10 AA.

AAU04532 ID AAU0 9 RESULT

셤 ð

Query Match

inflammation, especially rheumatoid arthritis, psoriasis and

diabetic retinopathy

Sequence 10 AA;

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the sequence represents a monomeric monocyclic peptide of the invention, whose 3 dimensional structure is modelled on the expose loop of human upone of the sequence of producing a monomeric monocyclic peptide by a measuring betamethed of producing a monomeric monocyclic peptide antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclising the cysteine residues. The monocyclic peptides and a cyclic peptide with at least one amino acid deleted prior cyclisation are used to interfere with angiogenesis, condition characterised by angiogenesis in envascularisation or lymphangiogenesis in a mammal with a condition or characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, peoriasis, nead, head, hormone-related angiogenic dysfunction, diabetes induced neovascular condition when an induced neovascular meaners in head, hypertension induced neovascular promoners are substanced angiogenic dysfunction, diabetes induced neovascular promoners in the properties of the monomers of the peptide of the monomers of the petide of the petide of the monomers of the petide of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection. The peptides are also uncontaints are infection. The peptides are also uncontaints in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity pleura, or brain. The peptides are used to inage blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents a monomeric monocyclic peptide of the invention,
                                                                                                                                                                  Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabeces induced neovascular sequelae; rheumatoid arthritis;

    .10
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                     diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cendron A;
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stacker S,
                                                                                                                          VEGF based monocyclic peptide 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                   Key
Disulfide-bond 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200152875-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2001.
                                                                          26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Achen MG,
                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues
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are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy

;

Gaps 5;

0; Indels

Score 41; DB 4; I Pred. No. 1.4e+06; 0; Mismatches 0;

67.2%; 81.8%;

Query Match
Best Local Similarity 81.00.

Sequence 9 AA;

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1 CISVPLISVPC 11

à 셤

6

CISVPL--VPC

Length

CISVPL-SVPC 10 CISVPLTSVPC 11

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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFO (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta petachen separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                        Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                     neovascularisation, lymphangiogenešis, psoriasis, tumour;
diabetes induced neovascular sequelae, rheumatoid arthritis;
diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                         /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cendron A;
                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 49; Page 32; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stacker S,
                                                                                                              VEGF based monocyclic peptide 11.
                          AAU04533 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                              16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                              L8-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2001; 2001WO-US001533
                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-442248/47.
                                                                                                                                                                                                                                                               Digulfide-bond
                                                                                                                                                                                                                                                                                                        WO200152875-A1.
                                                                                  26-SEP-2001
                                                                                                                                                                                                                                                                                                                                       26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Achen MG,
                                                                                                                                                                                                                     Synthetic
                                                        AAU04533;
RESULT 7
               AAU04533
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human UNGC VEGFD (vascular endothelial growth factor). The invention relates to a peta carbon separation distances on opposite antiparallel strands of a beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidiaing the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior or cyclisation are used to interfere with angiogenesis,

The condition of lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy, the condition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                             Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                     neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hughes RA, Stacker S, Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 49; Page 32; 102pp; English.
                                           AAU04529 standard; peptide; 9 AA.
                                                                                                                                                                                                  VEGF based monocyclic peptide 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200152875-A1.
                                                                                                                                                    26-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues.
                                                                                                   AAU04529;
RESULT 8
                             AAU04529
                                                                        to cyclisation are used to interfere with angiogenesis,

to cyclisation are used to interfere with angiogenesis,

characterised by angiogenesis in a mammal with a condition

characterised by angiogenesis, neovascularisation or lymphangiogenesis.

characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy,

characterised by angiogenesis, neovascularisation contropathy,

characterised by angiogenesis, neovasculariset testenosis, head, heat or cold

crebrovascular accident, post-angioplasty restenosis, head, heat or cold

crebrovascular peptides are also used to modulate vascular permeability

in a mammal (the mammal has a condition characterised by fluid

accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

crebrovasculature. The monomeric and biocyclic peptides are used to interfere

vith at least one biological activity induced by VEGF-C or -D and
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ARRSB412-42 are overlapping 8-mer peptides of the binding domain of TSAR (Totally Synthetic Affinity Reagents) peptide TSAR C46.9-2 (AARSB411). These bind (partially) a monoclonal antibody, ie. anti-CRA C46 (anticarcincembryonic antigen). TSAR peptides are generated using generic oligonucleotides (see AAQ/V470-73 for examples). TSARs are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or
                                                                                                                                                                                                                                                                                                 ö
            hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF, VBGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthitis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSAR; totally synthetic affinity reagent; synthetic; binding domain; effector domain; concatenated heterofunctional protein; linker; direct; rapid; detection; screening; treatment; monoclonal antibody; MAD; C46; anti-carcinoembryonic antigen; anti-CEA.
                                                                                                                                                                                                                                                                                                   Gaps
substance-induced neovascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                Score 32; DB 4; Length 9;
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial peptide 7 from TSAR C46.9-2 binding domain.
                                                                                                                                                                                                                                                           52.5%; scc...
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7.5; Page 108; 255pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR58418 standard; protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US000977.
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93US-00176500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-00189331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fowlkes DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-279739/34.
                                                                                                                                                                                                   diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                          3 SVPLTSV
                                                                                                                                                                                                                                                                                                                                                                             2 SVPLTSV
                                                                                                                                                                                                                                      Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1993;
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13-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR58418;
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                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR58418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid molecule comprising sequences encoding the CA125 protein, useful for diagnosing, preventing and/or treating cancer, e.g. ovarian, pancreatic, breast, endometrial or lung carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid molecule encoding an ovarian cancer antigen, CA125. Nucleic acid molecules, vaccine and methods are useful for diagnosing, preventing and treating cancer, e.g. pencreatic, lung, ovarian, breast or endometrial carcinoma. The invention is useful in gene therapy and as vaccines. The present sequence is CA125/MUC16 Oglycosylation site
a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or invivo antibody production. The TSARs are easily characterised and have designed activity allowing direct and rapid detection in a screening process. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 6; Length 9;
Pred. No. 1.4e+06;
0; Mismatches 2; Indel8
                                                                                                                                                                                Score 30; DB 2; Length 8; Pred. No. 1.4e+06; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA125; antigen; cancer; gene therapy; vaccine; MUC16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CA125/MUC16 O-glycosylation site #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 19; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                      AAE34703 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n
Similarity 75.0%;
6; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-2002; 2002WO-US014768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-MAY-2001; 2001US-0290480P
                                                                                                                                                                                      49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVPLTSVP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-129305/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yin BWT;
                                                                                                                                                                                                                                                  1 CISVPLTS 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVPTTSTP
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                1 CVSAPOTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200292836-A2
                                                                                                                                                             Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-NOV-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lloyd KO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m
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                                                                                                                                                                                                                                                                                                                                                                                        AAE34703;
                                                                                                                                 field.)
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                                                                                                                                                                                                                         Matches
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08-APR-1997

AAW12561;

RESULT 11 AAW12561 Synthetic.

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This sequence represents a core peptide of an src homology region 2 (SH2) binding peptide corresponding to the formula: 27-X-28-X X = any D- or L-amino acid; 27 = phosphotyrosine or its isostere; 28 = asparagine or its isostere; the amino terminus is acylated, and the peptide is less than 14 residues in length, with the proviso that if 27 is phosphotyrosine and 28 is asparagine, then the peptide is not GOZZYZSARLLL. SH2 binding peptides containing this core peptide are used to treat of diagnose diseases associated with aberrant cell growth, differentiation or regulation which is associated with defects in receptor tyrosine kinase pathways, by partially blocking or inhibiting a cellular signal transduction pathway. The disease may be cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent)
                                                                                                                  Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes; insulin-resistant diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS; lippoligosaccharide; monoclonal antibody; antibacterial; infection; antiinflammatory; meningococcal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 2; Length 11; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                  SH2 binding peptide core sequence #21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 117; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP47579 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gordon E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AFFY-) AFFYMAX TECHNOLOGIES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.2%;
71.4%;
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                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordeev MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-371373/37.
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Best Local Similarity
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2 CINVPFT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Szardenings AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                        31-JAN-1996;
                                           08-APR-1997
                                                                                                                                                                                                                                                                                    WO9623813-A1
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                                                                                                                                                                                                                                           Synthetic.
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AAW12615;
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ABP47579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AMM12551-70 represent core peptides of an src homology region 2 (SH2) binding peptide which correspond to the formula:

27-X-Z8-X X = any D- or I- amino acid; Z7 = phosphotyrosine or its isostere; Be asparagine or its isostere; the amino terminus is a sostere; Z8 = asparagine or its isostere; the amino terminus is a cylated, and the peptide is less than 14 residues in length, with the proviso that if Z7 is phosphotyrosine and Z8 is asparagine, then the peptides is not G827XZSYPLIL. SH2 binding peptides containing these core peptides are used to treat of diagnose diseases associated with aberrant cell growth, differentiation or regulation which is associated with cell growth, differentiation or regulation which is associated with cinhibiting a cellular signal transduction pathway. By partially blocking or inhibiting a cellular signal transduction pathway. The disease may be cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent) diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                        Core peptide; src.homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "given in the patent as pI, no further details given. May be intended to be phosphotyrosine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DB 2; Length 10;
Pred. No. 1.9e+02;
1; Mismatches 1; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hart CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grove JR,
                                                                                                                                                                                      SH2 binding peptide core sequence #11.
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW12615 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Page 116; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gordeev MF, Gordon E,
                                                    AAW12561 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFFY-) AFFYMAX TECHNOLOGIES NV.
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71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                             label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00382100.
                                                                                                                                                                                                                                                                                               insulin-resistant diabetes.
                                                                                                                                           (first entry)
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CISVPLT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Szardenings AK;
                                                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995;
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08-AUG-1996.

DΛ,

Patel

Kim MH;

Hart CP,

Grove JR,

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Gaps

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1; Indels

Query Match

RESULT 12 AAW12615 ID AAW1 XX

g ò

Voet P;

WO200228888-A2.

11-APR-2002

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The present invention describes mimotopes (I) of a surface L3, 7, 9, of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis
meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis
comprising a peptide epitope obtained by screening a peptide library with
comprising a peptide epitope obtained by screening and peptide library with
H44/78. (I) is antigenically cross-reactive with MAD. (I) have
H44/78. (I) is antigenically cross-reactive with MAD. (I) have
continued antiinflammatory activities, and can be used in
continued as medicament, and also in the manufacture of a medicament for
cuseful as a medicament, and also in the manufacture of a medicament for
treating or preventing meningococcal disease. (I) and MAB are useful for
treating a patient suffering from or susceptible to meningococcal disease
contracting meningococcal infection to detect antibodies against L3, 7, 9,
assay for meningococcal infection to detect antibodies against L3, 7, 9,
assay for meningococcal infection to detect antibodies against L3, 7, 9,
assay for meningococcal infection to detect antibodies against L3, 7, 9,
assay for meningococcal infection to detect antibodies against L3, 7, 9,
assay for meningococcal infection to detect antibodies against L3, 7, 9,
assay for meningococcal infection to detect antibodies against L3, 7, 9,
assay for meningococcal infection to detect antibodic against L3, 7, 9,
assay for meningococcal infection to detect antibodic sample from a patient. ANNB8464 to ABN88487 and ABP47336 to ABB47754
creptesent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding CAI resistance proteins - used in gene therapy, and for detecting CAI resistance in biological samples.
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                                                                                                                                                                                          Novel mimotope of Neisseria meningitidis surface, for treating meningococcal disease, comprising a peptide epitope obtainable by screening peptide library with a specific monoclonal antibody.
                                                                                           Poolman J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%; Score 29; DB 5; Length 11; 36.4%; Pred. No. 3.1e+02; tive 2; Mismatches 5; Indels
                                                                                           Letesson J, Lobet Y, Mertens PY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                             (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR77368 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                            Claim 15; Page 43; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liotta LA, Kim YS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-US003610.
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03-OCT-2000; 2000GB-00024200.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                       WPI; 2002-479596/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-1995;
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                                                                                                         De Bolle XT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kohn EC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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        ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes mimotopes (I) of a surface Li, 7, 9, of meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis
comprising a peptide epitope obtained by screening a peptide library with comprising a peptide epitope obtained by screening a peptide library with a monoclonal antipody (WAD) like 48B12C10, H44/24, H44/58, H44/70 or H44/78. (I) is antigenically cross-reactive with MAD. (I) have antipocterial and antihinflammatory activities, and can be used in antipocterial and antihinflammatory activities, and can be used in caseful as a medicament for useful as a medicament for treating or preventing meningococcal disease. (I) and MAB are useful for treating a patient suffering from or susceptible to meningococcal disease treating a patient suffering from to susceptible to meningococcal infection to detect antibodies against Li, 7, 9, and 10.05 and to detect the presence of Li, 7, 9 immunotype meningococcus in a completion a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754

represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS; lippoligosaccharide; monoclonal antibody; antibacterial; infection; antihiflammatory; meningococcal disease.
                                                                                                                                                                                                                                                                                                                                                       Voet
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel mimotope of Neisseria meningitidis surface, for treating meningococcal disease, comprising a peptide epitope obtainable by screening peptide library with a specific monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.5%; Score 29; DB 5; Length 11; 27.3%; Pred. No. 3.1e+02; tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                    De Bolle XI, Letesson J, Lobet Y, Mertens PY,
                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP47580 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 15; Page 43; 55pp; English
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                                                                                                                                                                                                        03-OCT-2001; 2001WO-BP011409.
                                                                                                                                                                                                                                                        03-OCT-2000; 2000GB-00024200.
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                     Neisseria meningitidis.
Synthetic.
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-479596/51.
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Sequence 11 AA;

11-APR-2002

Synthetic.

19-AUG-2002

ABP47580;

RESULT 14 ABP47580

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Gaps

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EXAMPLE 4; Page 40; 56pp; English.

XX

CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human CC melanoma cells, contains a unique proline-rich sequence which fulfills CC the consensus definition for Src homology 3 (SH3) binding proteins CC (AAR77366). 4 Unique versions (AAR77367-70) are present

XX

Squence 10 AA;
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Ouery Match 44.3%; Score 27; DB 2; Length 10; Best Local Similarity 62.5%; Pred. No. 6e+02; Matches 5; Conservative 0; Mismatches 3; Indels Qy 4 VPL/SVPC 11

Db 1 VPPAPVPC 8
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Search completed: March 8, 2004, 12:09:26 Job time : 53 secs

0;

0; Gaps

1.5.

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March 8, 2004, 12:10:46; Search time 33 Seconds (without alignments) 70:384 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809742 segs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listing first 45 summaries
                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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61
                                                                                                                                                                                                                                                                                                                                                                                                                1 CISVPLTSVPC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 11
                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Sequence 7, Appli	Sequence 23, Appl	Sequence 26, Appl	Sequence 24, Appl	Sequence 25, Appl	Sequence 13, Appl		Sequence 10, Appl	Sequence 332, App	Sequence 89, Appl	Sequence 11221, A	Sequence 11228, A	Sequence 11250, A	Sequence 11254, A	Sequence 11258, A
	QI	US-09-761-636A-7	US-09-761-636A-23	US-09-761-636A-26	US-09-761-636A-24	US-09-761-636A-25	US-09-761-636A-13	US-09-761-636A-14	US-09-761-636A-10	US-10-245-871-332					·	US-10-154-884B-11258
	DB	6	σ	Φ	σ	6	σ	σ	δ	15	14	15	12	15	12	15
	% Query Match Length DB	11	H	11	11	11	10	9	on	σ.	11	σ	6	6	. თ	6
	* Query Match	100.0	6.3	93.4	88.5	85.2	74.6	67.2	52.5	47.5	47.5	47.9	44	44	44.3	44.3
	Score	-19	50	57	54	2,5	45.5	41	32	50	29	80	22	27	27	27
	Result No.		0	ı	4	יני	9	7	α	o 0**	, -		12		1 -	15

Sequence 11259, A Sequence 11265, A Sequence 11275, A Sequence 20, Appl Sequence 20, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl Sequence 10, Appl Sequence 10, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 249, A	349, 464, 21, 2 250, 256,
US-10-154-884B-11255 US-10-154-884B-11265 US-10-154-884B-11280 US-10-154-884B-11280 US-10-38-862-20 US-10-38-862-20 US-10-88-33-245-1011 US-09-83-245-1011 US-10-166-151-19 US-10-166-151-19 US-10-166-151-19 US-10-166-151-19 US-10-166-151-12 US-10-166-151-12 US-10-166-151-12 US-10-166-113-5 US-09-866-135-5 US-09-866-135-5 US-09-866-135-5 US-09-761-636A-11 US-10-277-292-249 US-10-277-292-349 US-10-277-292-349 US-10-277-292-349 US-10-277-292-349 US-10-277-292-349 US-10-277-292-349	US-10-280-340- US-10-280-340- US-10-280-340- US-10-358-052- US-10-107-532- US-10-107-532-
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ALIGNMENTS

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patence 7. Application US/09761636A

patence 7. Application US/09761636A

patent No. US2002065218A1

GENERAL INFORMATION:

APPLICANT: ACHEN, Steven

APPLICANT: ACHEN, Steven

APPLICANT: TACKER, Steven

APPLICANT: TACKER, Steven

APPLICANT: THOREN, Angel

TITLE PREFERENCE: 1004/48505 Achen et al

TITLE PREFERENCE: 1004/48505 Achen et al

CURRENT FILING DATE: 2001-01-18

PRIOR PAPLICATION NUMBER: US 60/176,293

PRIOR PAPLICATION NUMBER: US 60/176,293

PRIOR PAPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

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PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR APPLICATION NUMBER: US
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Gaps

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RESULT 6
US-09-761-636A-13
Sequence 13, Application US/09761636A
Sequence 13, Application US/09761636A
Patent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: CENDRON, Angela
APPLICANT: CENDRON, Angela
STACKER: REFERENCE: 1064/486SC Achen et al
FILE REFERENCE: 1064/486SC Achen et al
CURRENT RPLING DATE: 2001-01-18
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR; FILE REFERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMERE: US/09/761,636A CURRENT FILING DATE: 2001-01-18; PRIOR FILING DATE: 2000-01-16

PRIOR FILING DATE: 2000-01-16

PRIOR FILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGP-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERENES: 1064/48505 Achen et al
CURRENT PLILAG DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR RILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERBION 3.0
SEQ ID NO 25:
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 11;
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                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 9; Length 11;
Pred. No. 0.03;
3; Mismatches 0; Indels
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Pred. No. 0.062;
3; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-761-636A-25; Septilication US/09761636A; Sequence 25. Application US/09761636A; Patent No. US20020065218A1; GENERAL INFORMATION:
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72.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25
                                                                                                                                                                                                                                                                                                                                                                                      88.5%;
72.7%;
                                                                                                                                                                                                                                                                                                                   ) ORGANISM: synthetic construct
US-09-761-636A-24
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Best Local Similarity 72.7
Matches 8; Conservative
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Matches 8; Conservative
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1 CISLPISSVPC 11
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1 CITIPLTSLPC 11
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US-09-761-636A-26

Sequence 26, Application US/09761636A

Pactent No. US20020065218A1

GENERAL INFORMATION:

APPLICANT: ACHER, Steven

APPLICANT: HUGHES, Steven

APPLICANT: HUGHES, Steven

APPLICANT: HUGHES, Steven

APPLICANT: GENERAL STACKER, Steven

APPLICANT: HUGHES, Steven

APPLICANT: GENERAL CENDOROW, ANGEL-D, VEGF PEPTIDOMIMETIC INHIBITOR

FILE REPERENCE: 1064/48505 Achen et al

CURRENT PELLING NATE: 2001-01-18

FILE RAPPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/176,293

PRIOR APPLICATION NUMBER: US 60/204,590

PRIOR PILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 34

SEQ ID NO 26

LENGTH: 11
                               GENERAL INFORMATION:
APPLICANT: ATTENEN, MATC
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
ITLE REPERENCE: 1064/48505 Achen et al
TITLE PEPERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT PILING DATE: 2000-101-18
PRIOR PILING DATE: 2000-101-18
PRIOR FILING DATE: 2000-01-16
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 11
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Best Local Similarity 81.8%; Pred. No. 0.01;
Matches 9; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 59; DB 9; Length 11;
Pred. No. 0.0049;
1; Mismatches 0; Indels
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; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
; CENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: synthetic construct
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US-09-761-636A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.7%;
Best Local Similarity 90.9%;
Matches 10; Conservative
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APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CISVPLTSVPC 11
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Sequence 33.2, Application US/10245871
| Sequence 33.2, Application No. US200323594A1
| Publication No. US200323594A1
| GENERAL INFORMATION:
| APPLICANT: HUMPRERSY, ROBERT
| TITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| PITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| PITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| PITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| PITLE OF INVENTION: II-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
| PRIOR APPLICATION WUMBER: US/10/17/00
| PRIOR FILING DATE: 2002-0-17
| PRIOR FILING DATE: 2002-0-14
| NUMBER OF SEQ ID NOS: 905
| SEQ ID NO 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: O'Mahony, Daniel J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Lambkin, Imelda J.
APPLICANT: Pinilla, Clemencia
APPLICANT: Houghten, Richard
TITLE OF INVENTION: WEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
TITLE OF INVENTION: WEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
TITLE OF INVENTION NUMBER: US/10/126,845
CURRENT APPLICATION NUMBER: US/10/126,845
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 99
LENGTH: 11
                                                                                                                                          Query Match 52.5%; Score 32; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 7.2e+05; Matches 7; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: MISC_FEATURE; LOCATION: (1)..(11); OTHER INPORMATION: D form retroinversion peptide US-10-126-845-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29; DB 15;
Pred. No. 7.2e+05;
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US-10-126-845-89
US-10-126-845-89
Figure 89, Application US/10126845
Fublication No. US20030181367A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRATURE:
OTHER INFORMATION: D form peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.5%;
Best Local Similarity 71.4%;
Matches 5; Conservative 1
; SEQ ID NO 10
; LENCTH: 9
; TYPE: PRT
; ORGANIEM: Homo sapiens
US-09-761-636A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT; ORGANISM: Homo sapiens
US-10-245-871-332
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2 VPITSTP 8
                                                                                                                                                                                                                                                     3 SVPLTSV 9
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APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: GENRON, Angela
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
TITLE OF INVENTION: VARGE-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR APPLICATION NUMBER: 3000-05-16
NUMBER: OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDEGN, Angela
APPLICANT: CENDEGN, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFRENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 9
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Pred. No. 7.2e+05;
0; Mismatches 0; Indels
       PRIOR FILING DATE: 2000-01-18
PRIOR APPLICANTION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.0
SEQ ID NO 13
LENGTH: 10
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Patent No. US20020065218A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
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Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                     74.6%;
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Best Local Similarity 90.9
Matches 10; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                       TYPE: PRT
CORGANISM: Homo sapiens
US-09-761-636A-13
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Gaps

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Length 9; 1; Indels

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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01351US
FILE REPERENCE: 014058-01351US
CURRENT PERILAGE NUMBER: US/10/154,804B
CURRENT FILING DATE: 2002-05-23
FRIOR FILING DATE: 2000-03-01
FRIOR FILING DATE: 2000-03-01
FRIOR FILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-05-01
FRIOR FILING DATE: 2000-05-04
FRIOR FILING DATE: 2000-05-04
FRIOR FILING DATE: 2000-05-04
FRIOR FILING DATE: 2000-05-04
FRIOR FILING DATE: 2000-05-03
FRIOR FILING DATE: 2000-05-04
FRIOR FILING DATE: 2000-05-03
FRIOR FILING DATE: 2000-06-03
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APPLICANT: Marnion, Jane
APPLICANT: Match Marc
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Thera,
TITLE OF INVENTION: Compositions and Malignancies
TITLE OF INVENTION: Hematchological Malignancies
FILE REFERENCE: 01458-01352105
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PLING DATE: 2000-03-01
PRIOR PLING DATE: 2000-03-01
PRIOR PLING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PLING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11250, Application US/10154884B Publication No. US20040005561A1 GRNERAL INFORMATION: APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Homo sapiens
US-10-154-884B-11228
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US-10-154-884B-11250
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APPLICANT: Rather, Marc W.
APPLICANT: Rather, Marc W.
APPLICANT: Coriza Corposations and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Composations and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: 014058-01321US
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR PRILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/180,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PRILING DATE: 2000-04-28
PRIOR PRILING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-01
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/220,003
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 200
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                                                                                           47.5%; Score 29; DB 14; Length 11;
45.5%; Pred. No. 2.7e+02;
Live 1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11221, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
APPLICANT: Giager, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
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1 CLLVPLLVAAC 11
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Best Local Similarity
Matches 4; Conserv
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2 CLSVPVS 8
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US-10-154-884B-11228
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US-10-154-884B-11221
                                                                                                               Query Match
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Matches
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GREARL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Marc W.
APPLICANT: Marc W.
APPLICANT: Marc W.
APPLICANT: Retear, Marc W.
APPLICANT: Retear, Marc W.
APPLICANT: Retear, Marc W.
APPLICANT: Coxixa Corporations and Methods for the Detection, Diagnosis and Therap TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap TITLE OF INVENTION: Hematological Malignancies
FILE REPERENCE: 01069-013-213
FILE REPERENCE: 2000-03-17
FILE REPERENCE: 2000-03-17
FILE REPERENCE: 2000-03-17
FILE REPERENCE: 2000-03-17
FILE REPERENCE: 2000-04-28
FILE REPERENCE: 2000-05-01
FILE REPERENCE: 2000-07-04-03
FILE REPERENCE: 2000-07-0
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Pred. No. 7.2e+05;
2; Mismatches 0; Indels
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                                                                                                                                                                              Sequence 11258, Application US/10154884B Publication No. US20040005561A1
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Best Local Similarity 66.7
Matches 4; Conservative
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US-10-154-884B-11258
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4 CLSVPV 9
                                                                                                                   RESULT 15
US-10-154-884B-11258
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US-10-154-8948-11254
US-10-154-8948-11254
Sequence 11254, Application US/10154894B
Sequence 11254, Application US/10154894B
Sequence 11254, Application US/10154894B
SPDICANT No. US20040005561A1
GENERAL INFORMATION: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: March, Marc W.
APPLICANT: Retreet, Marc W.
APPLICANT: Memoric March Hematological Malignancies
FILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352105
CURRENT FILING DATE: 2000-05-23
SPRIOR FILING DATE: 2000-05-23
SPRIOR FILING DATE: 2000-03-01
SPRIOR PAPLICATION NUMBER: US 60/186,126
SPRIOR APPLICATION NUMBER: US 60/186,126
SPRIOR APPLICATION NUMBER: US 60/200,545
SPRIOR APPLICATION NUMBER: US 60/200,999
SPRIOR FILING DATE: 2000-04-28
SPRIOR PLILING DATE: 2000-04-28
SPRIOR FILING DATE: 2000-04-28
SPRIOR PLILING DATE: 2000-05-04
SPRIOR PLILING DATE: 2000-05-04
SPRIOR FILING DATE: 2000-05-04
SPRIOR PLILING DATE: 2000-05-04
SPRIOR APPLICATION NUMBER: US 60/202,903
SPRIOR SPRIOR APPLICATION NUMBER: US 60/202,903
SPRIOR SPRIOR PLILICATION NUMBER: US 60/203
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       PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Mindows Version 3.0
SEQ ID NO 11250
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27; DB 15; Length 9; Pred. No. 7.2e+05; 2; Mismatches 0; Indels
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Best Local Similarity 66.73
Matches 4; Conservative
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Best Local Similarity 66.7%
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-10-154-884B-11250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CISVPL 6
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/cgm2_6/ptodata/2/iaa/fA_COMB.pep:*
/cgm2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptodata/2/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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72
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Maximum DB seq length: 13
                                                                                                                                                                                                                    Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 219, App Sequence 219, App Sequence 210, App Sequence 170, App Sequence 12, Appl Sequence 3, Appli Patent No. 5217669 Sequence 24, Appl Sequence 116, App Sequence 24, Appl Sequence 183, App Sequence 183, App Sequence 11, Appl Sequence 11, Appl Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 59, Appl Sequence 150, App Sequence 151, App Sequence 63, App] Sequence 63, App] Description Sequence 6 Sequence 6 Sequence 2 Sequence Seq US-09-042-107-63 US-09-722-114A-2 US-08-170-114A-2 US-08-170-114A-2 US-08-170-114A-2 US-08-160-513-70 US-09-258-754-219 US-09-258-754-219 US-09-228-702-219 US-09-428-082B-170 US-08-428-082B-170 US-08-65-54-4 US-08-65-54-4 US-09-627-775-24 US-09-2250D-183 US-07-214A-6 US-08-645-193B-7 US-08-645-193B-59 US-08-660-092-150 US-08-660-092-151 % Query Match Length DB Score Result No.

Sequence 152, App	Sequence 150, App	Sequence 151, App	Sequence 152, App	Sequence 91, Appl	Sequence 344, App	Sequence 30, Appl	Sequence 30, Appl	Sequence 35, Appl	Sequence 30, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 20, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 9, Appli	Sequence 1066, Ap	7501 0000:000	de 'eant annanhae	
US-08-660-092-152	US-09-160-513-150	US-09-160-513-151	US-09-160-513-152	US-08-250-789A-91	US-09-489-847-344	US-08-212-433A-30	US-08-716-256-30	US-09-069-827A-35	PCT-US95-03239-30	US-07-732-114A-1	US-08-170-114A-1	US-08-811-682-20	US-09-089-878-1	US-09-089-878-2	US-09-460-384-9	US-09-187-859-1066		US-09-839-542B-1066	
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28	29	0.6	9 (3.5	1 m	34	35	36	3.7	38	6	4	41	4.2	۲4	77	*	45	

ALIGNMENTS

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Sequence 63, Application US/09258754
; Sequence 63, Application US/09258754
; Patent No. 6174697
; GENERAL INFORMATION:
; APPLICANT: Rolatalini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; FILE REPRENCE: P. J. 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT PILING DATE: 1999-02-26
; EARLIER PILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: RNOBLAHLI, Erkki
APPLICANT: RNOBLAHLI, Erkki
APPLICANT: RNOBLAHLI, Renata
APPLICANT: RNOBLAHLI, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
TITLE OF INVENTION: 12892
CURRENT APPLICATION NUMBER: US/09/042,107
CURRENT PILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 436
SEQ ID NO 63
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-258-754-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h similarity 71.4%; Pred. No. 3e+05; 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 63, Application US/09042107
; Patent No. 6232287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 KSTNTFC 13
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US-09-042-107-63
US-09-258-754-63
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APPLICANT: KOTZIN, BRIAN L.
APPLICANT: MARRACK, PHILIPPA
APPLICANT: MARRACK, PHILIPPA
APPLICANT: RAPELER, JOHN
APPLICANT: PALIAND, XAVIER
TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNDEALING SOLDER:

UNDEALING SOLDER:

APPLICATION DATA:

APPLICATION NUMBER: US/08/170,114A

FILING DATE: 20-DECEMBER-1993

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US/08/172,114

PRIOR APPLICATION ADMER:

FILING DATE: 18-JULY-1991

PRIOR APPLICATION NUMBER: US/08/353

FILING DATE: 2-MARCH-1990

PRIOR APPLICATION NUMBER: US/08/353

FILING DATE: 2-MARCH-1990

PRIOR APPLICATION NUMBER: US/08/353

FILING DATE: 15-NOVEMBER-1999

APPLICATION NUMBER: US/08/353

FILING DATE: 15-NOVEMBER-1999

APPLICATION NUMBER: US/08/353

FILING DATE: 15-NOVEMBER-1999

ATORNEY AGART INFORMATION:

ANAME: ANAMER: 15-NOVEMBER-1999

ATORNEY AGART INFORMATION:

ANAME: ANAMER: 15-NOVEMBER-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.5%; Score 27; DB 1; L
54.5%; Pred. No. 2.1e+02;
tive 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 E. Prentice Avenue, Suite 200 CITY: Englewood STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Julie L. Bernard
REGISTRATION NUMBER: 36,450
REFERENCE/DOCKET NUMBER: NJH217.3
APPLICATION NUMBER: US/07/732,114A
          FILING DATE: 18-JULY-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/488,353
FILING DATE: 2-MARCH-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/437,370
FILING DATE: 15-NOVEMBER-1989
ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWAINSON
REGISTRATION NUMBER: 33,215
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEFANNE: (303) 850-9900
TELEFANNE: (303) 850-9901
TELEFANNE: (303) 850-9401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08170114A; Patent No. 5776708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
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GY: linear
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Best Local Similarity
Matches 6; Conserv
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US-09-722-250D-63
US-09-722-250D-63
Sequence 63, Application US/09722250D
Patent No. 6610631
GENERAL INPORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Rucelahti, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Tissues
CURRENT APPLICATION WHORE: US/09/722,250D
CURRENT FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 09/042,107
PRIOR FILING DATE: 1998-03-13
NUMBER OF EQ. ID NOS: 437
SEQ.ID NO 63
ENEMAR: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                  ; FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-042-107-63
                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                    1; Indels
                                                                                                                                                 Query Match
38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: KOTZIN, BRIAN L.
APPLICANT: WARRACK, PHILIPPA
APPLICANT: KAPPLER, JOHN
APPLICANT: PALIARD, XAVIER
TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07732114A Patent No. 5298396
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SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
Matches 5; Conservative
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3 RSTNTGC 9
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Gaps

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Sequence 70, Application US/09160513

Sequence 70, Application US/09160513

Patent No. 641075

GENERAL INFORMATION:
APPLICANT: Victoria, Baward J.
APPLICANT: Marquis, David M.
APPLICANT: Jones, David M.
APPLICANT: Jones, David S.
APPLICANT: W. Lin
APPLICANT: W. Lin
APPLICANT: W. Lin
APPLICANT: APL SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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| PATENT NO. 01.72074
| PATENT NO. 01.72074
| APPLICANT: Ruoslahti, Erkki
| APPLICANT: Rasqualini, Renta
| APPLICANT: Rajotte, Daniel
| TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
| TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
| TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
| TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
| FILE REFERENCE: P-LJ 3443
| CURRENT FILING DATE: 1999-02-26
| CURRENT FILING DATE: 1999-02-13
| NUMBER OF SEQ ID NOS: 452
| SERLIER FILING DATE: 1998-03-13
| NUMBER OF SEQ ID NOS: 452
| SECTION NOS: 452
| LENGTH: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FLORY
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,513
FILING DATE: 1998-DEC-24
CLASSIFICATION NUMBER: US/09/160,513
RATORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 25231-20061.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
US-09-258-754-219
; Sequence 219, Application US/09258754
; Patent No. 6174687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino_acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 36.1
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-160-513-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CASELGK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 chgvick 7
                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 70, Application US/08660092
| Sequence 70, Application US/08660092
| Patent No. 6207160
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Wictoria, Edward J. APPLICANT: Wictoria, Baylad M. APPLICANT: Wictoria, David M. APPLICANT: Willian Information: David M. APPLICANT: You, Lin ITILE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED ITILE OF INVENTION: PATHOLOGIES NUMBER OF SEQUENCES: 216
| CORRESPONDENCE ADDRESS: 216
| CORRESPONDENCE ADDRESS: MORELSON & FOERSTER STREET: 755 PAGE MILL ROAD STATE: CA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA
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Pred. No. 3e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                          37.5%; Score 27; DB 1; Length 13; 54.5%; Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,092
FILING DATE: 06-UNN-1996
FLING DATE: 06-UNN-1996
FLING DATE: 785-THE FREGATION:
NAME: Park, Freddis K.
REGISTRATION NUMBER: 35,636
REGISTRATION NUMBER: 35,636
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                             1; Mismatches
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71.4%;
TELECOMMUNICATION INFORMATION:
                       TELEPHONE: (303) 793-3333
TELEPAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 706141
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.1
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                              LENGIH: 13 amino acids
                                                                                                                                                                                                                                               Query Match 37.5
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-660-092-70
                                                                                                                                                                                                                                                                                                                                                 1 CASELGKSTNT 11
                                                                                                                                                                                                                                                                                                                                                                                               1 CASSLYGTRNT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CASELGK 7
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                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                   US-08-170-114A-2
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORGANISM: Artificial Sequence
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COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 4; Conservative
                  1 CASELGKSTNTFC 13
                                                                                          1 CGSHCGQLCKSLC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 NTFC 13
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US-08-182-967-12
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Patent No. 6610651

GENERAL INFORMATION:
APPLICANT: Rucelahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Molecules that Home to Various Selected Organs or TITLE OF INVENTION: Tissues
FILE REFERENCE: P-LJ 4514
CURRENT APPLICATION NUMBER: US/09/722,250D
CURRENT FILING DATE: 2000-11-22
PRIOR FILING DATE: 1998-03-13
NUMBER OF SEQ ID NOS: 437
COPPURABLE OF COPPURATION NUMBER: US 09/042,107
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US-09-042-107-219

US-09-042-107-219

Sequence 219, Application US/09042107

Sequence 219, Application US/09042107

SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 SEQUENCE 110 NOS: 436

SEQUENCE 110 SEQUENCE 120                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 38+02;
Matches 4; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                       Query Match
36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 7; Indels
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Pred. No. 3e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.1%;
Best Local Similarity 30.8%;
Matches 4; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 219
LENGTH: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CASELGKSTNTFC 13
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                                                                                                                                                                                                                                                                                                                                                                1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGSHCGOLCKSLC 13
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US-09-722-250D-219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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Sequence 12, Application US/08182967
Patent No. 6413516
GENERAL INFORMATION
APPLICANT: Chang, Jennie C.C.
APPLICANT: Chang, Jennie C.C.
APPLICANT: Carlo, Dennis J.
ITILE OF INVENTION: Peptides and Methods Against Psoriasis
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
NESULT 11
US-09-428-082B-170
Sequence 170, Application US/09428082B
Patent No. 6660843
GENERAL INFORMATION:
APPLICANT: FEIGE. URICH
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOOME, THOMAS CHARLES
TITLE OF INVENTION: MODIFED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/182,967
FILING DATE: 14-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/462,471
FILING DATE: 05-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/813,867
FILING DATE: 14-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: CALMODULIN ANTAGONIST PEPTIDE US-09-428-0828-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.1%; Score 26; DB 4;
100.0%; Pred. No. 3e+02;
tive 0; Mismatches 0
                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/428,082B
CURRENT FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR PILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 1133
SEQ ID NOS: 1133
SEQ ID NO 170
LENGTH: 13
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0;

Gaps

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Sequence 24, Application US/08866545
; Sequence 24, Application US/08866545
; Retent No. 626535
; GENERAL INFORMATION:
    APPLICANT: Greene, Mark I.
    APPLICANT: ANACHAI, Ramachandran
    APPLICANT: TAKASATI, Wataru
    APPLICANT: ANACHAICAN: PEPTIDE
    TITLE OF INVENTION: ANACHAICAGES DESIGNED FROM BINDING SITES OF TUMOR
    TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
    TITLE OF INVENTION: USES
    CORRESPONDENCES: 27
    CORRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5217869-110
;PREEDL NO. 5217869
;PREEDL NO. 5217869
;TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%; Score 24; DB 6; 57.1%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                               Score 24; DB 2;
Pred. No. 3e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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MEDIUM TYPER DISEcte
COMPUTER: DisEcte
COMPUTER: DisEcte
COMPUTER: DATABLE
OPERATING SYSTEM: DOS
SOFTWARE: FestSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,545
FILING DATE: 30-MAY-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 121
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
                                                                                                                                                                                                                                                                                         33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
                                                                                                                          SS: single
not relevant
                                                                                                                                                                                                                                                                                  33.3
Best Local Similarity 66.7
Matches 4; Conservative
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
                                                                                                                                                           TOPOLOGY: not relevar

MOLECULE TYPE: peptide

US-08-645-193B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GKSTNTF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                   8 STNTFC 13
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1 SFNSFC 6
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                                                                                               TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO:110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-866-545-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gotz, Friedrich
APPLICANT: Gotz, Friedrich
APPLICANT: Gotz, Friedrich
APPLICANT: Gotz, Friedrich
APPLICANT: Jung, Guncher, Christoph
APPLICANT: Jung, Guncher
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Mashington
STRATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24.5; DB 4; Length 12;
Pred. No. 5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Parentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/08/645,193B
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGRAT INPORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1540000
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELESPRONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                          APPLICATION UNDHAEN:

RILING DATE: 30-NAY-1990

PRIOR APPLICATION DATA:
APPLICATION UNDHER: US 07/382,085

FILING DATE: 18-UUL-1989

PRIOR APPLICATION DATA:
APPLICATION UNDHER: US 07/382,086

FILING DATE: 18-UUL-1989

PRIOR APPLICATION DATA:
APPLICATION UNDHER: US 07/326,314

FILING DATE: 21-MAR-1899

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Carlayn A.
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: 31,815

REFERENCE/DOCKET NUMBER: B-IM 9830

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

INFORMATION POR SEQ ID NO: 12:
ENGURNCE CHARACTERISTICS:
LENGTH: 12 aming acids
         APPLICATION NUMBER: US 07/644,611
FILING DATE: 22-03N-1991
PRIOR APPLICATION DATE: US 07/530,229
APPLICATION NUMBER: US 07/530,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08645193B Patent No. 5962253
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63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-182-967-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-645-193B-3
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6

Gape

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| ATTORNEY/AGENT INFORMATION:
| NAME: Coruzzi, Laura A | REGISTRATION NUMBER: 30,742 |
| REGISTRATION NUMBER: 30,742 |
| REFERENCE/DOCKET NUMBER: 009113-0004-999 |
| TELEPHONE: 650-493-4935 |
| TELEPHONE: 650-493-4556 |
| TOPOLOGY: 1 than on the following of the following o
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 8, 2004, 12:00:00; Search time 20 Seconds (without alignments) 38.477 Million cell updates/sec Run on:

US-09-761-636A-6 46 1 CNEESLIC 8 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283366 segs, 96191526 residues Searched: 605 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 8

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 1008

PIR 78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Description	jacalin beta-II ch		lipopeptide WS1279	calsequestrin, fas	metallothionein is	acylase - Kluyvera	ferredoxin a2 - Ja	dihydrofolate redu	Na+/K+-exchanging	galactose oxidase	aspartate kinase (traM protein - Bsc	R-phycoerythrin ga	glycoprotein compo	vicilin 57K chain	formylglycinamide		protein D - Escher	mitosis inhibiting	R-phycoerythrin al	fulicin - giant Af	dihydrofolate redu	venom heptapeptide	alpha-myosin heavy	variant surface gl	T-cell receptor be	pallidipin - assas	neuropeptide - sea	T-cell receptor be
		an T	829637	137263	JU0355	B39040	S59622	S19288	869165	B31263	S29881	XEYDGD	B47594	A32014	A37521	H48394	B34818	A12016	PC1002	A41890	A26830	B22565	A44692	A31263	A58512	I46868	C61512	PT0554	S55238	A60803	PT0610
		th DB	6	9	9	7 2	8	8	8	9	9	7 1	8	2	8	9	7	7 2	8	4 2	2	2	5	9	7 2	7 2	•	8	4	2	2
.	Query	Match Length	37.0	37.0	32.6	32.6	32.6	32.6	32.6	30.4	30.4	30.4	30.4	28.3	28.3	26.1	26.1	26.1	26.1	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	23.9	21.7	21.7	21.7
	,	Score	17	17	15	15	15	15	15	14	14	14	14	13	13	12	12	12	12	11	11	11	11	11	11	11	11	11	10	10	10
	Result	No.		7	m	4	5	9	7	60	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hydrogensulfite re tubulin beta-3 cha glutathione transf	hypothetical prote cadmium-binding he T-cell receptor be	Na+-transporting A globulin IV alpha	gene Cftr protein cytochrome P450 AL	tocopnerol-binding gene InIslow prote L-serine ammonia-l	R-phycoerythrin al metallothionein-A
S11556 S60293 S71870	S08606 B33882 PT0529	S45648 S09066 D61512	157018 A61597	S29272 I57532 A25836	A22565 I51049
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100	1999	999	222	222	თთ
30 31	9 9 9 1 2 4 9 1	36	0 8 4 0 0 0	4, 4, 4, L1 51 60	4 4 4 10

ALIGNMENTS

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jacalin beta-II chain - Artocarpus champeden (fragment)
jacalin beta-II chain - Artocarpus champeden
C;Deceise 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C;Accession: S29637
R;Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A;Pitle: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-3-A;Reference number: S29635; MUD:93152601; PMID:8427879
A;Accession: S29637
A
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A.Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine
C.Keywords: heterotetramer; lectin; seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 37.0%; Score 17; DB 2; Length 6; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C, Complex: heterotetramer; two alpha and two beta chains C; Punction:
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2 NEES 5 Š 셤

RESULT 2

Y protein - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C;Accession: I37263
R;Wabber, G: Habbener, J.F.
R;Wabber, G: Habbener, J.F.
Ridocrinology 131, 2010-2015, 1992
Ridocrinology 131, 2010-2015, 1992
R;Reference number: I37263, WUID:93010691, PMID:1396344
R;Reference number: I37263 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-6 <RES>

A;Cross.references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816 C;Genetics: A;Gene: CREB Gaps °, Query Match
37.0%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels

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C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Mar-1996
R;Peterson: Balliker, D.; Wellems, T.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988
A;Atile: Bxidence that a point mutation in dihydrofolate reductase-thymidylate synthase
A;Reference number: A94217; MUID:89057886; PMID:2904149
A;Accession: B31263
                                                                                                                                                                                                                                                                                                              acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Dacties: Kluyvera cryocrescens
C;Accession: S19288
R;Martin, J.; Slade, A.; Attken, A.; Arche, R.; Virden, R.
A;Title: Chemical modification of serine at the active site of penicillin acylase from A;Reference number: S19288; MUID:92109664; PMID:1764029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dihydrofolate reductase (BC 1.5.1.3) / thymidylate synthase (BC 2.1.1.45) - Plasmodium
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C;Species: Kaiware daikon (Japanese radish)
C;Species: Kaiwar-1998 #sequence_revision 10-Mar-1998 #text_change 17-Apr-1998
C;Dacession: S69168
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.
Arch. Blochem: Biophys. 316, 797-802, 1995-804, 1891-804
A;Title: Four ferredoxins from Japanese radish leaves.
A;Title: Four ferredoxins from Japanese radish leaves.
A;Reference number: S69164; MUID:95168867; PMID:7864635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.6%; Score 15; DB 2; Length 8; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Wolecule type: protein
A;Residues: 1-8 <OBA>
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein
Similarity 100.0%; Pred. No. 2.8e+05; 2; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.6%; Score 15; DB 2; I
40.0%; Pred. No. 2.8e+05;
rative 2; Mismatches 1;
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C;Keywords: methyltransferase; NADP; oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 32.6
Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>
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         Best Local !
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calsequestrin, fast skeletal muscle - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 23-Feb-1997
C;Accession: B39040
R;Cala, S.E.; Jones, L.R.
R;Cala, S.E.; Jones, L.R.
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein A;Reference number: A39040; MUID:91093153; PMID:1985907
                                                                                                                                                                                                                               C;Species: Streptomyces willmorei
C;Species: Streptomyces willmorei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000
R;Tsuda, Y:;Okada, Y:; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.
C;Accession: Juli: 39, 607-611, 1991
A;Title: Structure and synthesis of an immunoactive lipopeptide, WS1279, of microbial or A;Reference number: Juli: 39, 607-611, 1991
A;Reference number: Juli: 39, 607-611
A;Residues: 1-6 cTSU-
A;Note: the structure was confirmed by synthesis
A;Note: the structure was confirmed by synthesis
C;Ceywords: blocked amino end; lipoprotein
F;IAbiding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental
F;I/Modified site: fatty acylated amino end (Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metallothionein isoform a, cadmium-binding - Arianta arbustorum (terrestrial snail) (fra
C;Species: Arianta arbustorum
C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C,Accession: S59622
R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
Bocrger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.
Bocchem. J. 311, 951-957, 1995
A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothion A;Reference number: S59621; MUID:96067616; PMID:7487956
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A;Reaidues: 1-8 «BER»
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster
                                                                                                                                                                                                     lipopeptide WS1279 [validated] - Streptomyces willmorei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: protein
A;Resdiues: 1-7 <CAL>
C;Keywords: phosphoprotein; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 2; Conserv
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DB 2;

32.6%; Score 15;

Query Match

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glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (f C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cjaccession: H48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pi II-like sequences.
A;Reference number: A48394; MUID:93250576; PMID:8485470
                                                                                                                                                                                                                                                                                                                                                                                                R;Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.
J. Bacteriol. 170, 2749-2757, 1988
A:Title: Identification and characterization of the products from the traJ and traY ge:
A;Reference number: A32014; MUID:88227859; PMID:2836369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Spēcies: Gastroclonium coulteri
C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
C;Accession: A37521; J22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4895-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A;Reference number: A22565; MUID:85182601; PMID:3886644
                                                                                                                                                                                                                                                                                                        C;Species: Escherichia coli
C;Date: 22-Jun-1989 #sequence_revision 22-Jun-1989 #text_change 16-Feb-1997
C;Accession: A32014
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                                                              Score 14; DB 2; Length 8; Pred. No. 2.8e+05; 3; Mismatches 0; Indels
                                                                                                            3; Mismatches
                                                           30.4%;
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Similarity 66.7%;
2; Conservative 1
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50.0%;
  A,Residues: 1-8 <FOL>
C,Keywords: phosphotransferase
                                                                                     Best Local Similarity 40.09
Matches 2; Conservative
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A;Molecule type: protein
A;Residues: 1-8 <KLO>
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Best Local Similarity
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A,Genome: plasmid
C,Keywords: DNA binding
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Best Local Similarity
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-5 < INA>
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2 EEAVL 6
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A,Accession: protein
A,Molecule type: protein
A,Residues: 1-7 <ANI>
C,Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxid
C,Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxid
C,Superfamily: galactose oxidase inhibitor
C,Keywords: copper
                                                                                                                                                                                                                                                                                                        Rivalderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Briskin, D.P.
J. Biol. Chem. 260, 3852-3859, 1985
Afitie: Structural relatedness of three ion-transport adenosine triphosphatases around A; Reference number: S29881; MUID:85131201; PMID:3156136
A; Accession: S29881
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Experimental source: kidney
C.Keywords: ATP; heterodimer, hydrolase; ion transport; osmoregulation; phosphoprotein;
F;4/Active site: Asp (aspartylphosphate intermediate) #status predicted
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                                                                                                                                                                                                                 Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 19-Apr-2002
C;Accession: S29881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
C;Species: Cladobotryum dendroides
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
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                           Indels
  60.0%; Pred. No. 2.8e+05;
                         Mismatches
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                         Conservative
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R, Avigad, G.; Markus, Z.
Fed. Proc. 31, 447, 1972
A; Reference number: A01341
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2 CSDKT 6
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RESULT 15
B34838
vicilin 57K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Date: 10-Jul-1990 #sequence_revision 13-Sep-1993
A;Reference number: A34818
A;Reference number: A34818
A;Reference number: A34818
A;Accession: B34818
A;Accession: B34818
A;Accession: B34818
A;Accession: Dyeliminary
A;Molecule type: protein
A;Residues: 1-7 <MAN>
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A;Accession: H48394
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <MAT>
A;Residues: 1-6 <MAT>
A;Rote: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein
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Search completed: March 8, 2004, 12:03:35 Job time : 21 Becs

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March 8, 2004, 11:56:34; Search time 11 Seconds (without alignments) 37.869 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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46
1 CNEESLIC 8
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1		_	_		-		P13268 enterococcu	P80709 carcinus ma	P41495 Barcophaga			_	P82655 lactobacill		P38499 procambarus					P41863 calliphora	-		P80488 thiobacillu		P82618 periplaneta	P56575 rattus norv	P83195 perkinsus a		P58707 anthopleura			P41966 moniezia ex
SUMMARIES		TRM3 ECOLI	PLP_BRANA				FAR1_ASCSU	CAD1 ENTFA	ACT CARMA	TWOF SARBU	COW2 CONPU	GLUR HUMAN	ACPH RABIT	ASP2_LACSN	CCF1_ENTFA	FAR1 PROCL	GFRP MOUSE	WWA1 ACHFU	WWA3 ACHFU	FAR4_HOMAM			UH11_RAT	CLP THICU	CPDI ENTFA	PPK3 PERAM	UH09 RAT	WP1 PERAT		FLRN ANTEL	TPIS CANFA	UXA4 CHLTR	FARP_MONEX
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MEDINE=68227859; PubMed=2836369; Inamoto S., Yoshioka Y., Ohtsubo E.; Inamoto S., Yoshioka Y., Ohtsubo E.; "Identification and characterization of the products from the traJ and traY genes of plasmid R100."; J. Bacteriol. 170:2749-2757(1988).
i. FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION

Bacherichia coli. Plasmid IncFII R100. Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia. NCBI_TaxID=562;

RESULT 2
TRM3 ECOLI

1D TRM3 ECOLI

1D TRM3 ECOLI

No 1-JAN-1990 (Rel. 13, Created)

DT 01-JAN-1990 (Rel. 13, Last sequence update)

DT 01-JAN-1990 (Rel. 14), Last sequence update)

DT TRAM Protein (Fragment).

DE TrAM Protein (Fragment).

OS Escherichia coli.

OS Bacherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; En Colimon Colim

P81351 clostridium P22310 herpes simp P81805 carcinus ma P81808 carcinus ma P16101 alcaligenes P82101 litoria rub P83774 macrobrachi P3648 procambarus P41875 panagrellus P41866 calliphora P42884 leptinotars		s). Sordariomycetes; Hypomyces.	galactose oxidase from ecule but does not bind the mactivate the enzyme by	, Length 7; 05; 1; Indels 0; Gaps 0;
6 1 UNO6 CLOPA 6 1 VP19 HSV1K 7 1 ALL2 CARMA 7 1 ALL5 CARMA 7 1 CHOX ALCSP 7 1 EIOS_LITRU 7 1 FARZ PROCL 7 1 FARZ PROCL 7 1 FARZ CALVO 7 1 IANC CARUI 7 1 IANC CARUI 7 1 MNP1_LEPDE		dalactose oxidase inhibitori butylium dendroides (Cladobotryum dendroides) Bukaryota; Fungi; Ascomycota; Pezizomycotina; Hypocreomycetidae; Hypocreales; Hypocreaceae; NCBI_TaxID=5132;	eptide inhibitor of 1972). e copper ion per mol apoenzyme. It may in sthetic copper group inhibitor.	30.4%; Score 14; DB 1; larity 75.0%; Pred. No. 1.4e+05; Conservative 0; Mismatches 1 S 5
33.5 33.5 33.6 33.6 33.7 33.8 33.8 43.0 44.1 66.13.0 6	1 1 DACDE DACDE P06294; 01_JAN-1988 (Re 01_JAN-1998 (Re 01_OCT-1994 (Re	Galactose oxidase Dactylium dendroid Eukaryota, Fungi, Hypocreomycetidae, NCBI_TaxID=5132,	SEQUENCE. SEQUENCE. "Identification of a postylium dendroides." Fed. Proc. 31:447-447(Fed. 31:447-447(Fed. 31:447) FR. A01341; XEYDGD. COPPER: Metalloenzyme SEQUENCE 7 AA; 706	Query Match Best Local Similarity Matches 3; Conser 2 NEES 5
	RESULT IGAO DI LA PACE DE LA PACE	88888888	8	OME À A

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Gaps

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"Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANBOUS: On the 2D-gel the determined pI of this unknown protein is: 4.9, its MW is: 65 kDa.
SWISS-2DPAGE; P30087; HUMAN.
                                                                                                                                                                                   -!- MISCELLANEOUS: On the 2D-gel the determined pl of this unknown protein is: 5.1, its MW is: 36 kDa.

NON TER 7 7 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                        TISSUE=Fibroblast;
MEDLINE=95009907; PubMed=7523108;
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
"Separation and sequencing of familiar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";
Electrophoresis 15:735-745(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUR=Plasma;
MRDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Jeat sequence update)
11-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bromcheptapetic Imperial cone).
Evous imperialis (Imperial cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
                                                                                                                                                                                                                                                                   Score 12; DB 1; Length 7; Pred. No. 1.4e+05; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.1%; Score 12; DB 1; Length 8; 50.0%; Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA; 944 MW; C01772C455BB06DA CRC64;
                                                                                                                                                                                                                                      SEQUENCE 7 AA; 842 MW; 6AA72B1DDB1B1180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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1 HEEA 4
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28-FEB-2003 (
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ID UPA1 HUMAN
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                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pollen coat of Brassica napus.",
Planta 208:588-598(1999).
-!- FUNCTION: May play a structural role in the elaioplast, a tapetum-
specific plastidial lipid organelle.
-!- TISSUE SPECIFICITY: Tapetum of anthers.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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0
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             PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Uhknown protein from 2D-page of fibroblasts (P36) (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. TOPAZ; TISSUE=Tapetum;
MEDLINE=99349136; PubMed=10420651;
Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.3%; Score 13; DB 1; Length 8; 66.7%; Pred. No. 1.4e+05; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                   Score 13; DB 1; Length 5; Pred. No. 1.4e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 8 A3; 989 MW; 9D7B1AA452CAA042 CRC64;
                                                                                                                                                                                                                                                                          SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plastidial lipid-associated protein (Fragment).
Brassica napus (Rape).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA.
                                -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                        EMBL; M20941; -; NOT ANNOTATED CDS.
                                                                                                                                                                                                                                      Conjugation; Plasmid; DNA-binding.
                                                                                                                                                                                                                                                                                                          28.3%;
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Best Local Similarity
Matches 2; Conserv
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Matches 2; Conserv
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5 NDE 7
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P38641;
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PLP_BRANA
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Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
Baghdassarian D.,
A transabldolase. An enzyme implicated in crab steroidogenesis.";
Endocrine 5:23-23(1996).
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- SUBCELLUIAR LOCATION: Cytoplasmic.
-!- MISCELLARGOUS. ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
                                                                                                                                                                                 Sex pheromone CAD1.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria, Pirmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                               MEDLINE-85051889; PubMed-6437872; MEDLINE-85051889; PubMed-6437872; MEDLINE-85051889; PubMed-6437872; Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C., Craig R.A., Clewell D.B., Suruki A.; "Isolation and structure of the bacterial sex pheromone, cAD1, that induces plasmid transfer in Streptococcus faecalis."; FEBS Lett. 178:97-100(1984).
-!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PAD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinus maenas (Common shore crab) (Green crab).
Bukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;
Bubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 AA; 976 MW; 1424005AB2CAAEB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA; 819 MW; 047DD732C735B9C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.9%; Score 11; DB 1; I 66.7%; Pred. No. 1.4e+05; iive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10; DB 1;
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                     Ol_JAN_1990 (Rel. 13, Created)
Ol_JAN-1990 (Rel. 13, Last sequence update)
Ol-FEB-1991 (Rel. 17, Last annotation update)
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-1-SIMILIARITY: Belongs to the actin family.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin. like.
PROSITE; PS00405; ACTINS. 1; PARTIAL.
PROSITE; PS00432; ACTINS. 2; PARTIAL.
PROSITE; PS01132; ACTINS. ACTINE.
                                                                                 8 AA.
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50.0%;
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es 2; Conservative
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Best Local Similarity
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-!- FUNCTION: Potent modulator of inhibitory motorneurons. Reduces the input resistance and blocks slow oscillatory potentials in these
                                                                                                                                                                                                "A novel post-translational modification involving bromination of tryptophan. Identification of the residue, L.6-bromotryptophan, in peptides from Conus imperials and Conus radiatus venom.";
J. Biol. Chem. 272:4689(1997).
-!- FUNCTION: Does not elicit gross behavioral symptoms when injected centrally or peripherally in mice.
-!- SUBCELULIAR LOCATION: Secreted.
-!- SUBCELULIAR LOCATION: Secreted.
-!- TISSUB SPECIFICITY: Expressed by the venom duct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90180465; PubMed=2627377;
Cowden C., Stretton A.O.W., Davis R.E.;
"AFI, a sequenced bioactive neuropeptide isolated from the nematode
Ascaris suum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells.
--- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.
---- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
                                                                                             TISSUE-Venom;
MEDLINE-97184108; PubMed=9030520;
Craig A.G., Jimenez B.C., Dykert J., Nielsen D.B., Gulyas J.,
Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
McIntosh J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.9%; Score 11; DB 1; Length 7; 100.0%; Pred. No. 1.4e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11; DB 1; Length 7; Pred. No. 1.4e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                               Bromination; Amidation; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 6 BROMINATION.
7 7 AMIDATION.
7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 7 AAIDATION.
7 AA; 953 MW; 69D40059CB144350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                 SYNTHESIS, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FMRFamide-like neuropeptide AF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.9%;
larity 33.3%;
Conservative
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MOD_RES 7 7
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Matches 2; Conserv
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Best Local Similarity
                                            NCBI_TaxID=35631;
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Query Match

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Lote C.J., Weise J.B., Turning Of a low-molecular-weight highly polar Identification in urine of a low-molecular-weight highly polar glycopeptide containing cysteinyl-galactose."; Biochem. J. 123:25P-25P (1971).

Biochem. J. 123:25P-25P (1971).

Fig. A. 123:25P-25P (1971).

Biochem. J. 123:25P (1971).

Biochem. J. 
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MEDINTE=2922120; PubMed=1807161;
Krishna R.G., Chin C.C.Q., Wold F.;
"N-terminal sequence analysis of N alpha-acetylated proteins after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-MAY-2004 (Rel. 43, Last annotation update)
Acylamino-acid-releasing enzyme (RC 3.4.19.1) (AARE) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).
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Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                               1.4e+05;
les 0; Indels
                                                                                                                                              similarity 100.0%; Pred. No. 1.4e+05,
1; Conservative 0; Mismatches 0; Indela
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8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;
                                                                                          8 AA; 890 MW; 75A367672732CEB8 CRC64;
-!- SIMILARITY: Belongs to the contryphan family.
Toxin; Hydroxylation; D-amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                         D-LEUCINE
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                           Toxin; Hydroxylation; DISULFID 2 8
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Best Local Similarity
Matches 1; Conservat
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Homo sapiens (Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                            MOD RES
SEQUENCE
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GLUR HUMAN
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Matches
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01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
Trypsin-modulating oostatic factor (TMOF)
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; piptera; Brachycera; Muscomorpha; Oestroidea;
Sarcophagidae; Sarcophaga.
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MEDLINE=99388839; PubMed=10461743;
Jacobsen R.B., Jimenez B.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Regul. Pept. 50:61-72(1994).
-!- FUNCTION: Has an oostatic activity. Inhibite trypsin biosynthesis in the midgut which indirectly reduces the vitellogenin concentration in the hemolymph resulting in inhibition of oocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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J. Pept. Res. 54:93-99(1999).
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUB SPECTRIOTIY: Expressed by the venom duct.
-!- TASS SPECTROMETRY: MW-888.4; METHOD=LSIMS.
        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DEVELOPMENTAL STAGE: Synthesized and released from follicular epithelium after a blood meal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94211930; PubMed-8159807;
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conus purpurascens (Purple cone).

Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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          IndelB
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                           6 AA.
          Mismatches
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             Conservative
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P58785;
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SEQUENCE Query Match

Best Loc Matches

CONPU

COW2

RESULT 11

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Gaps

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completed: March 8, 2004, 12:02:10
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  SEQUENCE
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unblocking with N-acylaminoacyl-peptide hydrolase.";
Anal. Biochem. 199:45-50(1991).
-!- FUNCTION: This enzyme catalyses the hydrolysis of the N-terminal peptide bond of an N-acetylated peptide to generate an N-acetylated amino acid and a peptide with a free N-terminus. It preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.
-!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
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Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
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-i INDUCTION: Overexpressed in acid environments.
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Acid shock protein 2 (Fargment).

Actobacillus sanfranciscensis (Jactobacillus sanfrancisco).

Bacteria, Firmicutes, Lactobacillales; Lactobacillaceae;

Lactobacillus.
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                                                                                                                                                                                                                                                                      Score 8; DB 1; Length 6;
Pred. No. 1.4e+05;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                             6 AA; 775 MW; 6732D6C40B16F000 CRC64;
                                                                                               + peptide.
-!- SUBGINIT: Homotetramer.
-!- SUBCELLUAR LOCATION: Cytoplasmic.
-!- SIMILARITY: Belongs to peptidase family 89C.
PIR; A49792; A49792.
MEROPS; S09.004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P20104;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
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MEDLINE=21322712; PubMed=11429463;
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20.0%;
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2 ERQVL 6
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Matches
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CCF1 ENTFA
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MEDIJURE-89008313; PubMed=3139658; Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M., Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M., Mosit J.C., Dunny G.M., Suzuki A.; Structure of cefflu, a peptide sex pheromone which induces conjugative transfer of the Streptococcus faecalis tetracycline resistance plasmid, pCF10."; J. Biol. Cohen. 263.14574-14578 (1988).

J. Biol. Chen. 263.14574-14578 (1988).

HEMOLYSIN PLASMID PCF10.
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Pred. No. 1.4e+05;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                     SEQUENCE 7 AA; 790 MW;
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Best Local Similarity 33.33
Matches 1; Conservative
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RESULT 2
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Q67113 influenzavi
Q4264 fugur rubrip
Q4264 fugur rubrip
Q61984 rattus norv
Q32560 escherichia
Q92259 buchnera ap
Q9byy5 homo sapien
Q15995 homo sapien
Q15995 homo sapien
Q9bEQ2 ursus arcto
Q9bEQ2 ursus arcto
Q9bEQ2 macropus eu
Q9bEQ3 tragelaphus
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                                                        March 8, 2004, 11:59:40; Search time 38 Seconds (without alignments) 66.425 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                     1017041 segs, 315518202 residues
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Maximum Match 100%
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Q42564
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Q92Z39
Q98YY5
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sp_vinus:*
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sp_unclassified:*
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Gapop 10.0 , Gapext 0.5
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7 AA.

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sprague-Dawley;
MEDLINE=Sprague-Dawley;
MEDLINE=Sprague-Dawley;
Yoshikawa T., DuPont B.K., Leach R.J., Detera-Wadleigh S.D.;
Yoshikawa T., DuPont B.K., Leach R.J., Detera-Wadleigh S.D.;
Yoshikawa T., DuPont B.K., Leach R.J., Detera-Wadleigh S.D.;
Wew variants of the human and rat nuclear hormone receptor,
Expression and chromosomal localization of the human gene.";
Genmics 35:361-366(1996).
Genus, US9454; AAB9433.1; --
GO; GO:0004872; F:receptor activity; IEA.
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DJ107712.2 (Serine palmitoyltransferase, long chain base subunit
2-like (Aminotransferase 2), variant 1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.3%; Score 13; DB 11; Length 7; Best Local Similarity 100.0%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             30.4%; Score 14; DB 4; Length 8; 66.7%; Pred. No. 1e+06; ative 1; Mismatches 0; Indels
                                                                                                                                                                     Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL050320; CAD54807.1; -.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Orphan receptor TR4-NS (Fragment).
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Query Match
Best Local Similarity 66.'",
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                                                             Homo sapiens (Human)
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                                                                                                                                          SEQUENCE FROM N.A.
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1 VIC 3
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MEDLINE=97442476; PubMed=9285353;
Plummar N.W., McBurney M.W., Meisler M.H.;
Plummar N.W., McBurney M.W., Meisler M.H.;
Plummarive splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
LWO-domain protein in fetal brain and non-neuronal cells.";
EMBL; U97673; AAB80916.1; -.
GO; GO: GO: GO: Con channel activity; IEA.
                                                                                                                                                                                       MEDLINE-81001892; PubMed=7407922; Dhar R., Chancok R.M, Lai C.-U.; Pubmed R., Chancok R.M, Lai C.-U.; "Norviral oligonucleotides at the 5' terminus of cytoplasmic influenza viral mRNA deduced from cloned complete genomic sequences.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bureleostomi;
Actinoperygii, Neopterygii, Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acthropterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
                   01-NOV-1996 (TrEMBLrel. 01, Created)
1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annocation update)
Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   042564;
04-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
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                                                                                                           Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza A viruses.
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(TrEMBLrel. 23, Last sequence update)
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EMBL; M25045; AAA43202.1; -.
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Best Local Similarity
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                                                                                                                                             NCBI_TaxID=197911;
                                                                                                                                                                            SEQUENCE FROM N.A.
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Homo sapiens (Human)
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5 KSLV 8
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                                                                                                                                                                                             MEDLINE=99449059; PubMed=10520749; Hesslinger C., Sawers G.; Hesslinger C., Sawers G.; "The tdcg gene in Escherichia coli Will0 is separated from the rest of the tdc operon by insertion of IS5 elements."; DNA Seq. 9:183-188 (1999) EMBL; AJ001620; CAA04875.1; -. GMS, GO:0016301; F:kinase activity; IBA.
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                                                                                                             Bacteria, Protechacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Buchnera.
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A SIQUENCE FROM N.A.
A SIJUA F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
T "Structure and evolution of the leucine plasmids carried by the rendosymbiont (Buchnera aphidicola) from aphids of the family Applididea.

I FERS Microbiol. Lett. 168:43-49(1998).
R Microbiol. Lett. 168:43-49(1998).
R Microbiol. Lett. 168:43-49(1998).
R GO, GO:00038621; F.2.1sopropylmalate synthase activity; IEA.
M Lyase; Plasmid.
R GO, GO:0016829; F.1yase activity; IEA.
M Lyase; Plasmid.
R B
SEQÜENCE 8 AA; 917 MW; FE20S042D6CSB446 CRC64;
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
2_isopropylmalate synthase (EC 4.1.3.12) (Fragment)
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SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;
                                              01-JAN-1998 (TrEMBLrel 05, Created)
01-JAN-1998 (TrEMBLrel 05, Last sequence update)
01-JAN-19003 (TrEMBLrel 24, Last annotation update)
Propionate kinase (Fragment)
                        8 AA.
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TISSUE-Placenta;

A Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,

Loolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,

Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay B.A., Zhao Z.-Y.,

A Caskey C.T.H.;

"Isolation of chromosome-specific genes by reciprocal probing of a raryed consa and cosmid libraries.";

Taryed consa and cosmid libraries.";

EMBL, L32075; AAA73885.1; -.

TOWN TER 8 8

SEQÜENCE 8 AA; 921 MW; C6C735B33686ClAA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular phylogenetics and the origins of placental mammals.";
Nature 409:614-618(2001).
BMBL, AV01664; AAG4755.1; -.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0005635; F:DNA binding; NAS.
GO; GO:0006585; P:regulation of transcription, DNA-dependent; NAS.
SEQÜENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;
                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=21082082; PubMed=11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
CAMP responsive element moderator (Fragment)
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8 AA.
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PRT;
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Best Local Similarity 50.00,
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Query Match
Query Local Similarity 66./*,
Since 2; Conservative
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PRELIMINARY;
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RESULT 10 Q15890

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Eukāryota; Metazoa; Chordāta; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Tragelaphus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Echinops telfairi (Lesser hedgehog tenrec).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus. NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular phylogenetics and the origins of placental mammals.";
Nature 409:614-618(2001).
EMBL; AY011673; AAG47583.1; -.
                                                                                                                                                                                                                                                  "Molecular phylogenetics and the origins of placental mammals.";
Macure 409:614-618(2001).
EMBL; AV01621; AAG47536.1; -.
NON TER
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MEDLINE=21082082; PubMed=11214319;
Murphy W.J., Bizirik B., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brish N.J.,
                                                                                                                                                          [1]
MEDIZINE-21082082; PubMed-11214319;
MEDDINE-21082082; PubMed-11214319;
Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Erien S.J.;
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
cAMP responsive element moderator (Fragment).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) cAMP responsive element moderator (Fragment).
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                                                                                                                                                                                                                                                                                                                            8 AA; 978 MW; DFIDD331EEAB572A CRC64;
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(TrEMBLrel. 17, Last sequence update)
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                                                                              Macropus eugenii (Tammar wallaby).
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01-JUN-2001
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Q9BF90
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Q9BFB1
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TISSUE-Placenta.
Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
                                                                                                                                                              Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uraus arctos (Brown bear) (Grizzly bear).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Ursidae, Ursus.
                                                                                                                                                                                                                                                                                                                                  Caskey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of
arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0.0-0(1995).
EMBL: 132083; AAA73880.1; -.
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MURDLINE-21082082; PubMed=11214319;
MURDLYW.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A., O'Brien S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.1%; Score 12; DB 6; Length 8; 66.7%; Pred. No. 1e+06;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
cAMP responsive element moderator (Fragment).
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, Created)
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1-NOV-1996 (TrEMBLrel. 01, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
(Clone XP19G12A) (Fragment).
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SEQUENCE
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RESULT 12 Q9BFC2

Best Loca Matches

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
Balaenopteridae; Megaptera.
Mammalia, Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDDLINE-21082082; PubMed=11214319;
MURDLINE-21082082; PubMed=11214319;
MURDLINE-21082082; PubMed=11214319;
O'Brien S.J.;
"Molecular Dhylogenetics and the origins of placental mammals.";
"Mature 409:614-618(2001).
EMBL; AY011669; AAG47580.1; -.
NON_TER
                                                              MEDLINE=21082082; PubMed=11214319; Murphy W.J., Bizirik B., Johnson W.E., Zhang Y.P., Ryder O.A., O'Brien S.J., Do'Sten S.J., Dividence of the properties and the origins of placental mammals."; Nature 409:614-618(2001).

EMBL, AY011632; AAG47547.1; -.
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SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
0APP responsive element moderator (Fragment).
CREM.
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                  NCBI_TaxID=9371;
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March 8, 2004, 11:55:59; Search time 52 Seconds (without alignments) 43.469 Million cell updates/sec
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46
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A Geneseq 29Jan04:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ដ្	VEGF base	VEGF base	VEGF base	VEGF base	VEGF base	Conformat	Human CD4	Human TSH	Human TSH	Feline im	Peptide A	Protein p	Glutamine	Membrane	Endostati	Peptide C	Beta-2-mi	Human TSH	Human TSH	RGD-bindi	Membrane	Membrane	Membrane	Claudin-2	Integrin-
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SUMMARIES	QI	AAU04525	AAU04539	AAU04541	AAU04538	AAU04540	AAR24954	AAY54526	AAR73351	AAR73350	AAY57040	AAU08451	AAR80365	AAW49750	AAY48644	ABG35021	AAU08460	AAW25915	AAR73349	AAR73348	AAW12848	AAY48852	AAY48662	AAY48640	AAB06526	AAB17353
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d	Query Match	100.0	93.5	91.3	89.1	84.8	65.2	65.2	56.5	56.5	56.5	56.5	54.3	54.3	54.3	54.3	52.2	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
	Score	46	43	42	41	39	30	30	56	56	26	26	25	25	25	25	24	23	23	23	23	23	23	23	23	23
	Result No.	-	7	3	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aae08176 Peptide #	Aae08175 Peptide #	Abg34995 Human pro	Abg34987 Human pro	Aau81097 Integrin-	Abb72952 Integrin	Aar93979 Partial p	Aay64349 Cadherin-	Aay64350 Cadherin-	Aaw70546 Peptide 1	Aay48874 Membrane	Aay48637 Membrane	Aay48670 Membrane	Aay61125 Cadherin-	Aay64310 Cadherin-	Abj04389 HUVEC cel	Aay64348 Cadherin-	Aam52891 Plasmodiu	Aay62590 T-cadheri	Aay61019 Cadherin-
8 4 AAE08176	8 4 AAE08175	8 5 ABG34995	8 5 ABG34987	8 5 AAU81097	8 5 ABB72952	6 2 AAR93979	6 3 AAY64349	7 3 AAY64350	8 2 AAW70546	8 2 AAY48874	8 2 AAY48637	8 2 AAY48670	8 3 AAY61125	8 3 AAY64310	8 5 ABJ04389	5 3 AAY64348	5 5 AAM52891	6 3 AAY62590	6 3 AAY61019
23 50.0	23 50.0	23 50.0	23 50.0	23 50.0	23 50.0	22 47.8	22 47.8	22 47.8	22 47.8	22 47.8	22 47.8	22 47.8	22 47.8	22 47.8	22 47.8	21 45.7	21 45.7	21 45.7	21 45.7
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human, VEGF; vascular endothelial growth factor; angiogenesis; necvascularisation; Jymbhangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; theumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. AAU04525 standard; peptide; 8 AA. VEGF based monocyclic peptide 2. (first entry) 26-SEP-2001 AAU04525;

1. .8 /note= "This bond cyclises the peptide" Location/Qualifiers Key Disulfide-bond Synthetic.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533. WO200152875-A1. 26-JUL-2001.

Cendron A; Stacker S, (LUDW-) LUDWIG INST CANCER RES. Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VRGPD (vascular endothalial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet carbon separation distances on opposite antiparallel strands of a

Example 25; Page 47; 102pp; English.

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cyclising the peptide by oxidising the cysteine residues. The monocyclic cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, newsacularisation or lymphangiogenesis in meawal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, archeologian, vascularised malignant or benigh tumour, post-recovery cerebrovascular accident, post-engloplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive corrected angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability cor in a mammal (the mammal has a condition characterized by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic or brain. The peptides are used to image blood vessels and lymphatic or brain, inflammation, with an anti-inflammatory agent, to treat a conditional activity induced by VBGF. Or -D and care also used in combination with an anti-inflammatory agent, to treat a distance of inflammation, especially rheumatoid arthritis, psoriasis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 46; DB 4; Length 8; 100.0%; Pred. No. 1.4e+06; i.ve 0; Mismatches 0; Indels

    .8
/note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU04539 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JAN-2001; 2001WO-US001533.
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16-MAY-2000; 2000US-0204590P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8 AA;
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Matches
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to cyclisation are used to interfere with angiogenesis,
covacularisation or lymphangiogenesis in a mammal with a condition
characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Characterised by angiogenesis, neovascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriansis, arthropathy,
cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
confines. The peptides are also used to modulare vascular permeability
in a mammal (the mammal has a condition characterised by fluid
accumulation in peripheral limbs or in lungs, peritomeal cavity, pleura,
cor brain. The peptides are used to image blood vessels and lymphatic
cor brain. The peptides are used to image blood vessels and lymphatic
with at least one biological activity induced by VEGF- or -D and
care also used in combination with an anti-inflammatory agent, to treat a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                  The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endochelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.5%; Score 43; DB 4; Length 8; 87.5%; Pred. No. 1.4e+06; ive 1; Mismatches 0; Indels

    .8
/note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04541 standard; peptide; 8 AA.
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16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Query Match
Best Local Similarity 87.5..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8 AA;
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Cendron A;

Stacker S,

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Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neovascularisation, lymphangiogenesis, psoriasis, tumour; diabetes induced neovascular sequelae, rheumatoid arthritis, diabetic retinopathy; chronic inflammation; cyclic.

    .8
/note= "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                   Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF based monocyclic peptide 16.
                Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04538 standard; peptide; 8 AA.
(LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                       diabetic retinopathy
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CNEESVVC 8
                                                                                                                                                                                                                                                                                                                                                                   1 CNEESLIC 8
                              WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                      Sequence 8 AA;
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Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
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                                                                                                                                                                                                                      (LUDW-) LUDWIG INST CANCER RES.
                                                                                                18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                       16-MAY-2000; 2000US-0204590P.
                                                                                                                                               18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                                                                                                                          Hughes RA,
                                                                                                                                                                                                                                                                                                                      WPI; 2001-442248/47.
WO200152875-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8 AA;
                                                 26-JUL-2001.
                                                                                                                                                                                                                                                                          Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues.
  peptide loop fragment from an exposed loop of a growth factor protein and peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides dimeric bicyclic peptides (comprising 1 linked monocyclic peptides) and a cyclic peptides (comprising 1 linked monocyclic peptides) and a cyclic peptides with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, a condition characterised by angiogenesis, in mechasila with a condition characterised by angiogenesis, inecessis, arthropathy, recondition is diabetic retinopathy, psoriasis, arthropathy, recondition is diabetic retinopathy, psoriasis, head, head or cold trauma, substance-induced neconscular part research in the condition induced neconscular sequelae, or chronic liver sequelae, hypertension induced neconscular sequelae, or chronic liver in farmmal than a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to induse blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VGF-C or D and care also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                               Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                         The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to method of producing a mnomeric monocyclic peptide by a measuring beta beta carbon separation distances on opposite antiparallel strands of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.3%; Score 42; DB 4; Length 8; 75.0%; Pred. No. 1.4e+06; Live 2; Mismatches 0; Indels
                                                    Cendron A;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of human CC WGZPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betacce contains the peptide a monomeric monocyclic peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides loop factoric peptides with at least one residues. The monocyclic peptides and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis.

CC peptides and a cyclic peptide with a least one linked monocyclic peptides in a mammal with a condition are used to interfere with anglogenesis.

CC characterised by anglogenesis, neovascularisation or lymphanglogenesis.

CC characterised by anglogenesis, neovascularisation or lymphanglogenesis.

CC characterised by anglogenesis, neovascularisation of the liver, excessive createmer anglosenesis, neovascularisation of the liver, excessive corporation. The peptides are also used to modulate vascular permeability in fifection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, con brain. The peptides are used to inage hold vessels and lymphatic and contains are used to in a mammal of the interference.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. VEGF. or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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neovascularisation; lymphangiogenesis; psoriasis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.1%; Score 41; DB 4; Length 8; 75.0%; Pred. No. 1.4e+06; ive 2; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU04540 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy
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Best Local Similarity
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ID AAU0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *********
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26-JUL-2001

Synthetic.

Achen MG,

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Jarlais RLD, Dixon JS, Hendrickson WA, Kopple KD; noff CE, Ryu SE, Trunch A, Sweet RW;
                                                                                                                                                                                                                                                                                                                                                                                                        'note= "beta-turn or beta-turn mimic tetrapeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conformationally constrained peptides used for inhibiting HIV - \tilde{\rm b}_1 mimicking the stereochemical regions of the CD4 receptor protein.
                                                                                                                                                                      Human immunodeficiency virus; AIDS; envelope glycoproteins; CD4; cell surface protein; infection.
                                                                                                                                                                                                                                                                                                                                                            'note= "conformationally constraining gp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "conformationally constraining gp.
                                                                                                                               Conformationally constrained HIV inhibitory peptide
                                                                                                                                                                                                                                                                                            Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example, Page 24; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-00619782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91WO-US008873
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bhatnagar PK, Jarlais
Kwong P, Peishoff CE,
                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-217018/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CNEESLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNOGSFLC
                                                                                                                                                                                                                                                                                                   Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9209625-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39-NOV-1990;
                                                              25-MAR-2003
04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JUN-1992
                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                     AAR24954;
                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human by WegFP (vescular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a mesauring betabet a carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, peoritasis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold tramms collent period and analysis of the condition of the liver, excessive tramms, substance of mevascularisation of the liver, excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormone related angiogenic dysfunction, diabetes induced neovascular sequelae, bypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modilate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by WEGF. VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthitis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
  diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 4; Length 8;
Pred. No. 1.4e+06;
1; Mismatches 1; Indels
                                                                                                                                                              /note= "This bond cyclises the peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 25; Page 47; 102pp; English.
                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                    (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                L8-JAN-2000; 2000US-0176293P.
L6-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                     .8-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.v.,
6. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNEDSFIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-442248/47.
                                                                                                                     Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8 AA;
                                                                                                                                                                                                              WO200152875-A1
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The peptide is conformationally constrained by groups attached to each side. The peptide mimics a beta turn and can bind to at least one HIV envelope protein, thus inhibiting infection. It inhibits the interaction between HIV envelope glycoproteins and human cell-surface protein CD4 by mimicking structures of CD4. See also AAR24950-R24959 and AAR25122. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, CD4 protein; antigenic peptide; CDR2-like domain; apoptosis; syncytia formation; human immune deficiency virus; HIV binding;
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                      Score 30; DB 2; Length 8;
Pred. No. 1.4e+06;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human CD4 protein target antigenic peptide p1615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY54526 standard; peptide; 8 AA.
                                                                                                                                                                                                          65.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                               Local Similarity
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AAR24954 standard; protein; 8 AA.

RESULT 6 AAR24954 ID AAR2

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thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody; affinity; detection.
             thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody; affinity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.
                                                                                                                                                                                                                                                                                     Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.
                                                                                                                                                                                                                                                                                                                                                           Peptides with affinity to human TSH (thyroid stimulating hormone) receptor antibody are used for detection of the antibody. (See also AAR73201-592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides with affinity to human TSH (thyroid stimulating hormone) receptor antibody are used for detection of the antibody. (See also AAR73201-592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 2; Length 8;
Pred. No. 1.4e+06;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MITP ) MITSUBISHI PETROCHEMICAL CO LID.
                                                                                                                                                                                                                     (MITP ) MITSUBISHI PETROCHEMICAL CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TSH receptor (residues 291-298).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 25; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                  Example 1; Page 25; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR73350 standard; peptide; 8 AA.
                                                                                                                                                         93JP-00240853.
                                                                                                                                                                                       93JP-00240853.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93JP-00240853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-167251/22.
                                                                                                                                                                                                                                                     WPI; 1995-167251/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CNEESL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CNESSM 6
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP07089991-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1993;
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                                                                                           JP07089991-A.
                                                                                                                                                         28-SEP-1993;
                                                                                                                                                                                       28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-APR-1995.
                                                                                                                           04-APR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR73350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR73350
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a target antigenic peptide derived from the CDR2-like domain of the human CD4 protein. The peptide is cyclised by the addition of cystein eresidues at either end. The specification of cascribes antigenic peptides derived from the CDR2-like domain of CD4 (amino acids 27-66 of AAY54500). These antigenic peptides present cutralising receptor/Co-receptor effectors sites of the CDR2-like domain. The peptides evoke effective antibody responses by having optimised sitespecificity. The induced antibodies block human immune deficiency virus specificity. The induced antibodies block human immune deficiency virus corrections with other cells, deliver signals to T cells (inhibiting normal CD4+mediated immunoregulatory functions) or induce apoptosis of corrections with other cells, deliver signals to T cells (inhibiting normal CD4 cells by simultaneous engagement of T cell receptors. Conjugates and peptides containing the antigenic peptides are used for active immunisation to generate antibodies against CD4 surface complexes, especially to prevent binding of HIV to CD4 and thus HIV infection, but also to treat undesirable immune responses such as transplant rejection, or autoimmune diseases (theumatodia arthritis, systemic lupus autoimmune diseases (theumatodia arthritis, systemic lupus antibodies which are broadly neutralising against primary isolates from all lasses of HIV-1 and of HIV-2. The peptides may include a promiscuous T helper epitope that is active in genetically diverse subjects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                        /note= "this peptide is conformationally restricted by cyclisation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  New antigenic peptide from the CDR2 domain of CD4, for immunization against e.g. human immune deficiency virus.
CD4-Class II interaction; immunisation; CD4 surface complex; immune response; transplant rejection; autoimmune disease; cyclic; rheumatoid arthritis; systemic lupus erythematosus; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65.2%; Score 30; DB 3; Length 8; 50.0%; Pred. No. 1.4e+06; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human TSH receptor (residues 301-308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 63; 106pp; English.
                                                                                                         Location/Qualifiers
1..8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR73351 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                        (UNBI-) UNITED BIOMEDICAL INC.
                                                                                                                                                                                                                                                                                        98US-00100409.
                                                                                                                                                                                                                                                        99WO-US014030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-160579/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                 Key
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                          21-JUN-1999;
                                                                                                                                                                                                                                                                                        20-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-1995
                                                                                                                                                                                           W09967294-A1
                                                                                                                                                                                                                          29-DEC-1999,
                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR73351;
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                                                                                                                                                                                                                                                                                                                                                        Wang CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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ID AAR3

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AC AAR3

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DT 12-1

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DE Hume
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Gaps

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AAY57040;

RESULT 10

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The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the polynectostides encoding them, and their use for identifying agents that colymucleotides encoding them, and their receptors. VEGFs and their modulate interactions between VEGFs and their receptors VEGFs and their receptors play an important role in vasculogenesis, the development of the embryonic vasculations from early differentiating endothelial cells and angiogenesis, the process of forming new blood vessels from precentising ones. Modulators of interactions between VEGF and its receptors existing ones. Modulators of interactions between VEGF and its receptors of spaces. Such disorders include cancers, abnormal angiogenesis, proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique receptor binding profiles compared to known naturally occurring VEGFs.

ANUGH446-AAUGH445 represent the peptides Al-A9 which are encoded by human VEGF-A forward primers used in the methods of the present invention
                                                                                                                         Human; vascular endothelial growth factor; VEGF-A; vasculogenesis; angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis; age-related macular degeneration; rheumatoid arthritis; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptides that bind cellular receptors for vascular endothelial growth factors, polynucleotides encoding them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein polymeric adhesion substrate glutamine donor peptide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 26; DB 4; Length 8; Pred. No. 1.4e+06; 1; Mismatches 1; Indels
                                                                                        Peptide A6 encoded by human VEGF-A forward primer A6-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR80365 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Fig 7C; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES. (LICH ) LICENTIA OY.
                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-2000; 2000US-0185205P.
18-MAY-2000; 2000US-0205331P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.5%;
                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US006113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 66.77,
Best Local 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alitalo K, Jeltsch MM;
                                                                                                                                                                                           primer; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-536640/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CNEESL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CNDEGL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS12807
                                                                                                                                                                                                                                                                                          WO200162942-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-1996
                                                                                                                                                                                                                                   Bapiens.
                                                     21-NOV-2001
                                                                                                                                                                                                                                                                                                                                30-AUG-2001.
                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR80365;
                    AAU08451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR80365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            田城北城市諸田
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is an immunogenic fragment of feline immunodeficiency virus (FIV) glycoprotein 130. Peptides AAY57038-Y57039 (also fragments of gp130) are used in the invention as capture polypeptides when diagnosing FIV infection. The invention relates to an antibody binding composition which consists of an enhanced capture polypeptide, which contains an immunogenic fragment of FIV gap precursor p55, and a second fragment which is part of the env precursor gp130, and an antibody-binding detection composition. The invention also includes a device for performing an assay which determines whether a feline is infected with Immunodeficiency Virus infection
                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             Feline immunodeficiency virus; FIV; infection; diagnosis; gpl30; p55; immunogenic fragment; antibody; env precursor; gag precursor; cat; antibody binding composition.
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                     Score 26; DB 2; Length 8;
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26; DB 3; Length 8;
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Feline immunodeficiency virus immunogenic fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing Feline Immunodeficiency Virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'connor TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 4; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU08451 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                          AAY57040 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feline immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0085615P.
98US-00089878.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99EP-00303760.
                                                       56.5%;
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                                                                                            4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IDEX-) IDEXX LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mermer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-025671/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                       Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                                                                                      1 CNEESL 6
                                                                                                                                                          CNESSM E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8 AA;
                    Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP962774-A1.
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Groat RG,

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Gaps

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Query Match

Matches

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RESULT 11 AAU08451 ID AAU08

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This is an example of a glutamine donor peptide that can be utilised in novel recombinant protein polymers of the invention. Such polymers (see AAM4910-28) typically comprise a repetitive amino acid backbone of repetitive units having a collagen, fibroin, elastin or keratin motif and at least 2 enzyme recognition sequences comprising a glutamine and/or lysine capable of enzyme catalysed isopetide formation. The polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. They can be used as medical adhesives and sealants, in the closure of wounds and repair of damaged tissues, prosthesis coatings, drug depots, and matrices for the transplantation of cells. (Updated on 25-WAR-2003 to correct PF field.)
                                                                                       New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives and sealants, depots and matrices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP; prostate; ovary; lymph node; adrenal gland; liver; gut; tumour; membrane dipeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 2; Length 8; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Membrane dipeptidase-binding lung homing peptide #15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruoslahti EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 144; 193pp; English
                                                                                                                                                                         Example 9; Col 49; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY48644 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.3%;
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Best Local Similarity 37.5%,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-571717/48.
                                                     WPI; 1998-387091/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : :||
CGQSKVIC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1998;
26-FEB-1999;
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10-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1999
              Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY48644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY48644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptides AAR80351-70 are examples of glutamine donor peptides which can be used to generate protein polymeric adhesion substrate (PPAS) contay repeats of non-fibrin cross-linking donor peptide sequences (see AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be used as substrates in enzymatic cross-linking reactions catalysed by a transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair
              Pendent group, repeating unit, enzyme recognition site; sealant, fibrin, enzymatic cross-linking; biocompatible material, structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                              Protein polymers comprising repeating units and sequences - capable of enzyme-catalysed covalent bond formation useful as a biocompatible material for wound closure and tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein polymer; adhesive sealant; wound healing; cross-linking.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 2; Length 8; Pred. No. 1.4e+06; Aismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                             (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                         protein polymer adhesive substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 9; Page 75; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW49750 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.3%;
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                                                                                                                                                                                                                                                                       94US-00205518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Slutamine donor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-320413/41.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 AA;
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                                                                                                                                                      W09523611-A1
                                                                                                                                                                                                                                  3-MAR-1995;
                                                                                                                                                                                                                                                                       03-MAR-1994;
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12-OCT-1998
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                                                                                                                                                                                           08-SEP-1995
                                                                                                                                                                                                                                                                                                                                                    Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                  Synthetic.
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RESULT 13 AAW49750

Matches

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This invention relates to a novel method for identifying disease targeting peptides. The method comprises exposing a sample from an organ, tissue or cell type of interest, to a phage display library and recovering phage bound to the sample (the phage expresses targeting peptides). The peptides identified by the method of the invention may have cytostatic, immunosuppressive, anti-inflammatory, antiathritic, antiatherosclerotic, antidiabetic, antibaterial and antiviral activities. The methods and composition are useful for identifying targeting peptides and one or more receptors for a targeting peptide. The targeting peptides are used for selective delivery of therapeutic agents, including gene therapy vectors and fusion proteins, to specific organs, tissues, or cell types in subject. The targeting peptide may also be used
                                                                                                                                                                                                                                                                           .;
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              tissue or organ. The peptides can be used for identifying an organ or tissue or for treating an target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver and lymph node. The peptide bind to the membrane dipeptidase (MDP). AAV48618 to AAV49066 represent sequences which are used in the exemplification of the present invention. (Updated on 20-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Targeting peptide, cancer, Hodgkin's disease, cytostatic; immunosuppressive; anti-inflammatory; antiarthritic; antiviral; antiatheroscleroric; antidiabetic; antibacterial; diabetes mellitus; inflammatory disease, arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection.
                                                                                                                                                                                                                                                                             Gaps
present invention describes peptides that selectively home to a
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                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                   Score 25; DB 2; Length 8; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 56; Page 242; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG35021 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Endostatin targeting peptide #20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001; 2001WO-US027702
                                                                                                                                                                                                                                      54.3%;
50.0%;
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                                                                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arap W, Pasqualini R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-383050/41.
                                                                                                                                                                                                                                                                                                                  CNEESLIC 8
                                                                                                                                                                                                                                                                                                                                         | |:| |
1 CGNETLRC 8
                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                Sequence 8 AA;
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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for treating diseases such as diabetes mellitus, inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and viral infections and Hodgkin's disease. The present sequence represents a targeting peptide of the invention
                                                                                                                                                     Gaps
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                                                                                                                   Score 25; DB 5; Length 8;
Pred. No. 1.4e+06;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                     Search completed: March 8, 2004, 12:01:47
                                                                                                                      54.3%;
37.5%;
                                                                                                                                                       3; Conservative
                                                                                                                                       Similarity
                                                                                                                                                                                      1 CNEESLIC
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                                                                                         Sequence 8 AA;
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Best Local S
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                                                                                                                                                                                           March 8, 2004, 12:03:05; Search time 33 Seconds
(without alignments)
51.189 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_MRW_PUB_pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_MRW_PUB_pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB_pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB_pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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46
1 CNEESLIC 8
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Match Length
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Perfect
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SUMMARIES

SUMMARIES

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SCORE Match Length DB ID

Description

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SCORE Match Length DB ID

Outry

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US-09-761-636A-20 ; Sequence 20, Application US/09761636A ; Patent No. US20020065218A1

RESULT 2

Sequence 1071, Ap Sequence 3624, Ap Sequence 3624, Ap Sequence 3663, Ap Sequence 3663, Ap Sequence 3663, Ap Sequence 242, App Sequence 2242, App Sequence 2246, App Sequence 2246, App Sequence 2246, App Sequence 2246, App Sequence 36, App Sequence 3609, App Sequence 3609, App Sequence 3609, App Sequence 2160, App Sequence 2160, App Sequence 2143, App Sequence 214, App Sequence 2240, App Sequence	HN	Length 8; Indels 0; Gaps 0;
8 14 US-10-006-869-1071 8 15 US-10-006-869-3624 8 15 US-10-395-032-1071 8 15 US-10-395-032-1663 5 14 US-10-006-869-3663 5 15 US-10-006-869-3663 6 14 US-10-006-869-2865 6 15 US-10-006-869-2246 6 15 US-10-006-869-2246 7 14 US-10-006-869-2246 7 15 US-10-395-032-2246 7 15 US-10-395-032-2246 8 13 US-10-035-032-2246 8 14 US-10-035-032-2246 8 14 US-10-035-032-2246 8 14 US-10-1144-1175 8 14 US-10-1144-1175 8 14 US-10-1140-164-39 8 14 US-10-106-869-2160 8 14 US-10-106-869-2160 8 14 US-10-106-869-3160 8 14 US-10-106-869-3160 8 15 US-10-395-032-160 8 15 US-10-395-032-160 8 15 US-10-395-032-160 8 15 US-10-395-032-160 8 15 US-10-395-032-143 8 15 US-10-369-226-143 8 15 US-10-06-869-993 5 14 US-10-06-869-993	ALICNMENTS n US/09761636A 118A1 cc Steven tichard Angela Angel	100.0%; Score 46; DB 9; 100.0%; Pred. No. 7.2e+05; vative 0; Mismatches 0; 8
22 22 22 22 22 22 22 22 22 22 22 22 22	1. 1 636A-6 ence 6, Applicat nt No. US2002006 tral INFORMATION LICANT: STRACKE LICANT: STRACKE LICANT: GTRACKE LICANTON LE OF ILING DATE: COR PILING DATE:	Ouery Match Best Local Similarity Matches 8, Conser Matches 1, CNESSIC 1 CNESSIC 1 CNESSIC
11111010101010101010101010101010101010	RESULT US-09-09-09-09-09-09-09-09-09-09-09-09-09-	Query Best J Matche Qy Db

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; Sequence 21, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
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75.0%;
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                                                                                                                                                                                                                                                                                                                                           h 89.1%;
Similarity 75.0%;
6; Conservative
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Best Local Similarity 75.0 Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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US-09-795-006A-133
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US-09-761-636A-21
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; GENERAL INFORMATION:
    APPLICANT: ACHEN, Marc
    APPLICANT: ACHEN, Marc
    APPLICANT: HUGHES, Richard
    PILE REFRENCE: 1064/48505 Achen et al
    CURRENT TAPLICATION NUMBER: US 60/176,293
    PRIOR APPLICATION NUMBER: US 60/176,293
    PRIOR PILING DATE: 2000-01-18
    PRIOR PILING DATE: 2000-01-18
    PRIOR PILING DATE: 2000-05-16
    NUMBER OF SEQ ID NOS: 34
    SOSTABRE: Patentin version 3.0
    TEMPORE. Patentin version 3.0
    TEMPORE.
APPLICANT: ACHEM, Marc
APPLICANT: ACHEM, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFREMENCE: 1064/48650 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PARCHING NOS: 34
SOFTWARE: PARCHIN VERSION 3.0
SEQ ID NO 20
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Pred. No. 7.2e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 93.5%;
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity
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1 CNEESVVC 8
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US-09-761-636A-19
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Patent No. US20020151680A1
GERREAL INFORMATION:
APPLICANT: Alitalo et al
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: MATERIAL GROWTH FACTOR DNAS AND PROTEINS
TITLE OF INVENTION: NOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
TITLE OF INVENTION: S0077185.006A
CURRENT APPLICATION NUMBER: US/09/795,006A
PRIOR APPLICATION NUMBER: US 60/205,331
PRIOR APPLICATION NUMBER: US 60/205,331
PRIOR APPLICATION NUMBER: US 60/205,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STACKER, Steven
APPLICANT: GTACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
APPLICANT: HUGHES, Richard
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US 60/1761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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TITLE OF INVENTION: VEGF-D/VEGF PEPTIDOMIMETIC INHIBITOR FILE REPERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: 02/09/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR APPLICATION NUMBER: US 60/176,293 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-16 NUMBER: US 60/204,590 PRIOR FILING DATE: 2000-05-16 NUMBER: PARIOR FILING DATE: 2000-05-16 SEQ ID NOS: 34 SOFTWARE: PATENTIN VERBION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 9; Length 8; Pred. No. 7.2e+05; 2; Mismatches 0; Indels
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Pred. No. 7.2e+05;
1; Mismatches 1;
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Gaps

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RESULT 10
US-09-185-908-115
Sequence 115, Application US/09185908A;
Publication No. US20020193294A1
GENERAL INFORMATION:
APPLICANT: Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
TITLE OF INVENTION: FUNCTIONS
TITLE OF INVENTION: USON FUNCTIONS
TITLE OF INVENTION: UNDER: US/09/185,908A
                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; ; OTHER INFORMATION: peptide
US-09-827-345-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 23; DB 9; Length 8; Best Local Similarity 37.5%; Pred. No. 7.2e+05; Matches 3; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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APPLICANT: FRIES, ULRICH
APPLICANT: KOHNO, TADAHIKO
APPLICANT: LACEY, DAVID LES
APPLICANT: BOONE, THOMAS CHARLES
TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
FILE REFERENCE: A-68GA
CURRENT PILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: 60/198,919
PRIOR PELING DATE: 2000-04-21
PRIOR PELLING DATE: 2000-04-21
PRIOR FILING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 135
SEQ ID NOS: 135
SEQ ID NO 25
LENGTH: 8
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Pred. No. 7.2e+05;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: PCT/FR96/01006
PRIOR FLIANG DATE: 1996-06-28
PRIOR PLIANG DATE: 1998-02-19
PRIOR PELICATION NUMBER: PS 95/07914
PRIOR APPLICATION NUMBER: FR 95/07914
PRIOR APPLICATION NUMBER: FR 95/07914
PRIOR PELIANG DATE: 1995-06-30
NUMBER OF SEQ ID NOS: 28
SEQ ID NO 14
LENGTH: 7
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                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 80.09
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Sequence 14, Application US/09827345

Publication No. US20030021800a1

GENERAL INFORMATION:

APPLICANT: GENERALN, JEAN-CLAUDE

APPLICANT: GALEA, PRSCALE

TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN

TITLE OF INVENTION: UNTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND

TITLE OF INVENTION: UNTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND

TITLE OF INVENTION: DIAGNOSIS

TITLE OF INVENTION: UNBERS: US/09/827,345

CURRENT APPLICATION NUMBER: US/09/827,345

CURRENT PAPLICATION NUMBER: 09/599,549

PRIOR FILING DATE: 2000-06-23
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Patent No. US20020151680A1

GENERAL INFORMATION:

APPLICANT: Alitalo et al

TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS

FILE REPERENCE: 28967/35979B

CURRENT APPLICATION NUMBER: US 60/205,331

PRIOR PILIAGE DATE: 2001-02-26

PRIOR PILIAGE DATE: 2000-02-18

PRIOR PILIAGE DATE: 2000-02-18

PRIOR PILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 175

SOFTWARE: PATENTIN VERY 2000-02-25

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OTHER INFORMATION: Description of Artificial Sequence: synthetic
THER INFORMATION: peptide
US-09-795-006A-142
                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
CTHER INFORMATION: peptide
US-09-795-006A-133
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66.7%; Pred. No. ...
... 0; Mismatches
                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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        PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.79,
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TYPE: PRT ORGANISM: Artificial sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                     3; Conservative
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Best Local Similarity
Matches 3; Conserv
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1 CNEKT 5
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US-10-006-869-3665
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US-10-190-082-92
LENGTH: 6
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; Fublication No. US20030229199A1
; GENERAL INCORMATION; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: GOUY, BATBARA J.
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFREENCE: 1000686.407C9
; CURRENT APPLICATION NUMBER: US/10/395,032
; CURRENT FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100096,4077
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT APPLICATION NUMBER: US/12-03
SOFTWARE: PATENTING DATE: 2001-12-03
SOFTWARE: PATENTING US: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Representative cyclic modulating agent based on "OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion CTHER INFORMATION: recognition sequence US-10-006-869-3664
                                                                                                                                                     FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Product of
OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
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                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                       Query Match 50.0%; Score 23; DB 9; Length 8; Best Local Similarity 37.5%; Pred. No. 7.2e+05; Matches 3; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3664, Application US/10006869 Publication No. US20030082166A1 GENERAL INFORMATION:
                                                                                                                                                                                                                     FEATURE:
, OTHER INFORMATION: Cyclic Peptide
US-09-185-908-115
    CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 60.0%,
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US-10-006-869-3664
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; Sequence 3665, Application US/10006869;
; Publication No. US20030082166A1;
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.;
; APPLICANT: Gour, Barbara W.;
; APPLICANT: Gour, Barbara W.;
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL;
; TITLE OF INVENTION: CADHERIN MEDIATED FUNCTIONS
; FILE REFERENCE: 100066.4077;
; CURRENT FILING DATE: 2001-12-03
; CURRENT FILING DATE: 2001-12-03
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
OTHER INFORMATION: recognition sequence
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47.8%; Score 22; DB 14; Length 7;
Best Local Similarity 60.0%; Pred. No. 7.2e+05;
Matches 3; Conservative 2; Mismatches 0; Indels
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| Sequence 92, Application US/10190082
| Publication No. US20030148264A1
| GRNERAI INPOWNATION:
| APPLICANT: Lasky, Lawrence A.
| APPLICANT: Sidhu, Sachdev S.
| APPLICANT: Held, Heike A.
| TITLE OF INVENTION: PHAGE DISPLAYED FDZ DOMAIN LIGANDS
| FILE REFERENCE: P1905R1
| CURRENT APPLICATION NUMBER: US 60/303,634
| PRIOR APPLICATION NUMBER: US 60/303,634
| PRIOR FILING DATE: 2002-07-05
| WUMBER OF SEQ ID NOS: 683
| SEQ ID NO 92
| LENGTH: 7
                                                                                                                                                                                                                                             47.8%; Score 22; DB 15; Length 6; 60.0%; Pred. No. 7.2e+05; Live 2; Mismatches 0; Indels
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US-10-190-082-92

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US-10-395-032-3665
US-10-395-032-3665
US-10-395-032-3665
Squence 3665, Application US/10395032
Publication No. US20030229199A1
GREERAL INPORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE PREPRENCE: 100086.407C9
CURRENT APPLICATION UNDERR: US/10/395,032
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SSOTWARR: PatentIn Ver. 2.0
SEQ ID NO 3665
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ORGANISM: Artificial Sequence
PRATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
US-10-395-032-3665
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Query Match
Best Local Similarity 57.1%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 2; Indels
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1 CNEKT 5
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115, App (7, App 115, App 114, App 114, App 114, App 114, App 113, App 114, App 115, App 115, App 116, App 117, App 117, App 118, Ap

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| Sequence 2726, Application US/09187859A
| Sequence 2726, Application US/09187859A
| Patent No. 6386920
| GENERAL INFORMATION:
| APPLICANT: Blaschuk, Orest W.
| APPLICANT: Blaschuk, Orest W.
| TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
| TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
| FILE REPRESENCE: 100068.4072|
| CURRENT PALLICATION NUMBER: US/09/187,859A
| SEQ ID NOS: 4052
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NOS: 2726
| LENGTH: 9
| TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-2 cell adhesion recognition sequence
US-09-535-852-1681
                                                                                                                      Sequence 3
Sequence 1
Sequence 1
 Sequence (Sequence Sequence (
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Patent No. 6638911
GENERAL INPORMATION:
APPLICANT: Blachuk, Ozest W.
APPLICANT: Blachuk, Ozest W.
TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
TITLE OF INVENTION: DESMOSCWAL CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: DESMOSCWAL CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2000-05-21
NUMBER OF SEQ. ID NOS: 2009
SOFTWARE: PREENCE OF WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
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US-09-357-952-67

US-09-357-552-115

US-09-521-650-115

US-09-521-650-115

US-09-168-888-67

US-09-168-888-115

US-09-357-952-114

US-09-357-952-114

US-09-357-952-113

US-09-37-952-113

US-09-37-952-113

US-09-168-888-113

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Best Local Similarity
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  US-09-187-859-2726
                                                                                                                                                                                                                                                                                         US-09-535-852-1681
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   LENGTH: 9
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8, Appl
116, App
68, Appl
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                                                                                March 8, 2004, 12:16:07; Search time 15.5 Seconds
(without alignments)
29.976 Million cell updates/sec
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1. /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*

2. /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*

3. /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*

4. /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*

5. /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*

6. /cgn2 6/ptodata/2/iaa/backfiles1.pep:*

6. /cgn2 6/ptodata/2/iaa/backfiles1.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-187-859-2726

US-09-819-5428-2726

US-08-189-331-147

US-08-189-331-148

US-08-189-331-149

US-08-189-331-149

US-08-189-331-150

US-08-189-331-150

US-08-471-068-149

US-08-471-068-149

US-08-471-068-149

US-08-471-068-149

US-09-150-150

US-09-150-150

US-09-150-150

US-09-157-919

US-09-168-888-69

US-09-168-888-69

US-09-168-888-69

US-09-521-650-69

US-09-521-650-68

US-09-521-650-116

US-09-521-650-116

US-09-521-650-116

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1 CISVPLVPC 9
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Match Length
                                                             protein search,
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Perfect score:
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Patent No. 5747334
GENERAL INFORMATION:
APPLICANT: Kay, B. K. APPLICANT: FOWIKES, D. M. TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.2%; Score 24; DB 1; Length 7; 60.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: COUNTENTIN, APERICATION
OF THE CONTINENTING THE COUNTRY APPLICATION NUMBER: US/08/189,331
APPLICATION NUMBER: US/08/189,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-AUG-1991
ATTORNEY/ABERT INFORMATION:
REGISTRATION NUMBER: 30330
TELECOMMUNICATION NUMBER: 216-275P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,206A
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NAME: Mistock, S. Leelie
REGISTRATION NUMBER: 18,972
REFERENCE FOOCKET NUMBER: 1101-
TELEPHONE: 212 790-9090
TELEPRA: 212 86-8864/9741
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                  TELEFAA:
TELEX: 248345
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
"""DOILOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Conservative
                                                                                                                                                                                                                                                                                             703-241-2848
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: unknown;
MOLECULE TYPE: peptide
US-08-189-331-147
                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-261-206A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: Concur
CLASSIFICATION: 435
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Best Local Similarity
Matches 3; Conserv
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2 PVAPC 6
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US-08-189-331-147
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APPLICANT: BLASCHUK, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CAMPERIN' MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Ratentin Ver. 2.0
SEQ ID NO 2726
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
                                                     OTHER INPORMATION: Representative cyclic modulating agent based on OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
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APPLICANT: Suzuki, Koji
APPLICANT: Suzuki, Koji
APPLICANT: Matsuda, Abi
APPLICANT: Matsuda, Abi
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: with Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ABICAL, Stewart, Kolasch & Birch
ADDRESER: Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 26; DB 4; Length 9; 44.4%; Pred. No. 3e+05; tive 2; Mismatches 3; Indels
                                                                                                                                                                                        3; Indels
                                                                                                                                            Query Match 50.0%; Score 26; DB 4; Length 9; Best Local Similarity 44.4%; Pred. No. 3e+05; Matches 4; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22046-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 N. Washington St. CITY: Falls Church STATE: Virginia COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                        US-09-839-542B-2726
; Sequence 2726, Application US/09839542B
; Patent No. 6569996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18, Application US/08261206A
Patent No. 5574007
GENERAL INFORMATION
APPLICANT: Zushi, Mitichitaka
APPLICANT: Yamamoto, Shuji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
            ORGANISM: Artificial Sequence
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Best Local Similarity
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                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: CONCULTENTLY herewith
                                                                                                                                                                                                                                                                                                FILING DATE: Concurrently here CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REPERENCE/DOCKET WUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELEPRAX: 212 869-8864/9741
TELERX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Conservative
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MOLECULE TYPE: peptide
US-08-189-331-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 3; Conserv
                             STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
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New York
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US-08-189-331-150
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Patent No. 5747334
GENERAL INFORMATION:
APPLICANT: FOWLES, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.2%; Score 23; DB 1; Length 8; 60.0%; Pred. No. 3e+05;
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                          44.2%; Score 23; DB 1; Length 8; 60.0%; Pred. No. 3e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/189,331
FILING DATE: Concurrently herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCY/CALCY NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEFAX: 212 790-9090
TELEFAX: 212 669-864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                Sequence 148, Application US/08189331
Patent No. 5747334
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60.0
Matches 3; Conservative
                          Query Match
Best Local Similarity 60.0
Matches 3; Conservative
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MOLECULE TYPE: peptide
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New YOLK
STATE: New YOLK
TOTAL OF THE STATE
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1101-155
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,072
REFERENCE/DOCKET NUMBER: 1101-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 190-9090
TELERAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CISVP 5
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US-08-471-068-148
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US-08-471-068-147
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NIWA, MINEO
APPLICANT: STITO, YOSHINASA
APPLICANT: BUINA, TAKAO
APPLICANT: ISHII, YOSHINORI
APPLICANT: ISHII, YOSHINORI
TITLE OF INVENTION: A NEW CEPHALOSFORIN C ACYLASE
NUMBER OF SEQUENCES: 64
CORRESPONDENCES: 04
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23; DB 1; Length 8;
Pred. No. 3e+05;
3; Mismatches 1; Indels
                                                                                                                                                       Query Match 44.2%; Score 23; DB 1; Length 8; Best Local Similarity 60.0%; Pred. No. 3e+05; Matches 3; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparation-
OPERATING SYSTEM: PC-COMPATE:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CHRRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,760
FILING DATE: 01-MAY-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNATION:
NAME: OBLON, NORWAN F.
REGISTRATION NORWAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-929-0 PCT
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 413-220
TELEX: 248655 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08633760
Patent No. 5804429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 42.9
Matches 3; Conservative
  SEQUENCE CHARACTERISTICS
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                      1 CISVP 5
                                                                                                                                                                                                                                                                            1 CVSAP 5
                                                                                                                    US-08-189-331-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-633-760-9
                                                                                                                                                                                                                                                                                                                                                           JS-08-633-760-9
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RESULT 10

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Gaps
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Fatent No. 5948635
GENERAL INFORMATION
THORMATION:
APPLICANT: FOWIKes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTR: New York
COUNTR: New York
COUNTR: New York
COUNTR: REAGABLE FORM:
MEDIUM TYPE: FIOPDPy disk
MEDIUM TYPE: FIOPDPy disk
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC Compatible
COMPUTER: IEM PC COmpatible
COMPUTER: IEM PC COMPATION: SYSTEM: PC-DOS/MS-DOS
Sequence 147, Application US/08471068
Patent No. 5948635
GENRAL INFORMATION:
APPLICANT: FOWINES D. M.
TITLE OF INVENTION: TOtally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.2%; Score 23; DB 2; Length 8; 60.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                              STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
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Сарв
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                                                                                                                                                                                                                                                                                                                                      Sequence 150, Application US/08471068
Fatent No. 5948635
GENERAL INFORMATION:
APPLICANT: Kay, B. K.
APPLICANT: Kay, B. K.
APPLICANT: Townkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 186
CORRESPONDENCE ADDRESS:
ADDRESSED: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STREET: New York
COUNTRY: US.A.
ZIP: 10036-2211
                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.2%; Score 23; DB 2; Length 8; 60.0%; Pred. No. 3e+05; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
COMPUTER READABLE PCPM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRETT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
                                                                                                                      Score 23; DB 2;
Pred. No. 3e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1101-155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-
TELEPHONE: 212 790-999
TELEFAX: 212 86-9864/9741
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 150:
SEQUENCE CHRACTERISTICS:
LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 4, Application US/08891271; Patent No. 6165476
                                                                                                                      44.2%;
                                                                                                                                                                  3; Conservative
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Matches 3; Conservative
                                    TOPOLOGY: unknown;
MOLECULE TYPE: peptide
US-08-471-068-149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-150
  TYPE: amino acid
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                                                                                                                         Query Match
Best Local Similarity
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1 CVSAP 5
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                                                                                                                                                                                                         1 CISVP 5
                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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US-08-891-271-4
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Sequence 149, Application US/08471068

Patent No. 5940-1508

Patent No. 5940-1508

APPLICANT: Kay, B.K.

APPLICANT: Kay, B.K.

TITLE OF INVENTION: Totally Synthetic Affinity Reagents

NUMBER OF SEQUENCES: 186

CORRESPONDENCE ADDRESS.

ADDRESSES: Pennie & Râmonds

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.2%; Score 23; DB 2; Length 8; 60.0%; Pred. No. 3e+05; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
PatentIn Release #1.0, Version #1.25
                                                                                                                                                       ATTLING CALE
NAME: ANGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCS/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEFROME: 212 79-99-99
TELEFROME: 212 79-99-99
TELEFROME: 212 86-884/9741
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 148:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
FILING DATE:
                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/189,331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212 869-8864/9741
TELEX: 66414 PENINE
INFORMATION FOR SEQ ID NO: 149:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 60.(
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown;
MOLECULE TYPE: peptide
US-08-471-068-148
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: ILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: New York COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CISVP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CVSAP 7
                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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CONTINUE STATEMENT BY PREMATICANT: STATEMENT, ATTAIN TO STATEMENT BY PRAILINGART: STATEMENT, ATTAIN TO STATEMENT, ATTAIN TO STATEMENT, ATTAIN TO STATEMENT S
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Query Match

44.2%; Score 23; DB 3; Length 9;

Best Local Similarity 80.0%; Pred. No. 3e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PIVPC 9

Db 4 PLVAC 8

Search completed: March 8, 2004, 12:21:09

Job time: 16.5 Becs
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Page

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March 8, 2004, 11:52:24; Search time 20 Seconds (without alignments) 62.524 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                            1827
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       283366 segs, 96191526 residues
                                                                     using sw model
                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                            1 CASELGKSTNTFC 13
                                                                                                                                                                          US-09-761-636A-5
72

    protein search,

                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 13
                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                              Scoring table:
                                                                OM protein
                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

		•4≎				
Result No.	Score	Query Match	Length	DB		Description
1	33.5	46.5	12	2	PT0216	T-cell recentor be
7	30	41.7	12	~	S47394	-cell antigen r
m	29.5		13	7	S47357	-cell antigen
4	29		12	~	S26549	-cell receptor
Ŋ	28		12	7	PH1463	1 receptor
Q	28		12	~	PH1466	-cell receptor
7	28		13	~	S47400	-cell
œ	27		11	~	PT0217	-cell
თ	27	37.5	12	7	S47391	_
10	27		13	~	S47383	_
11	26	36.1	11	ď	857575	l receptor
12	56	36.1	12	7	847395	$\overline{}$
13	7	36.1	13	7	S47381	-cell antigen
14	25.5	35.4	13	7	S47382	1 antigen
15	25		10	7	S23371	_
16	25		11	~	PH0947	T-cell receptor be
17	25		12	7	PH1469	-cell receptor
18	N		12	~	PH0931	receptor
19	24.5		12	~	PH1457	receptor
20	24		11	~	PH1583	hain V-D-J
21	24		12	~	S26552	[e]
22	24	33.3	12	N	S26559	T-cell receptor be
23	24	33.3	12	~	S26554	l receptor
24	24	33.3	12	7	S47363	l antigen r
25	24		12	7	PH1467	-cell
56	24	ښ	12	~	PH1468	-cell receptor
27	$^{\circ}$		13	~	S47390	-cell antigen r
28	23.5	32.6	12	7	PH1459	
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T-cell receptor be	T-cell receptor be	T-cell receptor be	н	•	T-cell receptor be	_		T-cell receptor be		T-cell antigen rec	antigen	receptor	receptor	_	
S26557	S26556	S26553	PH1462	PH1470	PH1464	A23695	S26541	PH1458	S47356	S47378	S47385	PH0927	S26546	S26547	\$26555
7	7	~	7	7	~	~	7	~	7	7	~	~	~	~	N
12	12	12	12	12	12	13	12	12	13	13	13	10	12	12	12
31.9	31.9	31.9	31.9	31.9	31.9	31.9	31.2	31.2	31.2	31.2	31.2	30.6	30.6	30.6	30.6
23	23	23	23	23	23	23	22.5	22.5	22.5	22.5	22.5	22	22	22	22
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

```
T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C;Accession: PT0216
R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restr
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Reference town PT0216
A;Redecule type: mRA
A;Residues: 1-12 < NAXA
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell antigen receptor VJ junction beta chain - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-dan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: 847394; 847369
R;Lehner, P.J.
Submitted to the EMEL Data Library, August 1994
A;Reference number: 847355
A;Reference number: 847355
A;Accession: 847394
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-12 cLEH:
A;Cross-references: EMEL:235714; NID:9527523; PIDN:CAA84783.1; PID:9527524; EMEL:23569:
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                            Ή,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                     Query Match 46.5%; Score 33.5; DB 2; Length 12; Best Local Similarity 72.7%; Pred. No. 12; Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 2;
Pred. No. 51;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.7%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CASSLG-TINT 10
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
S47357
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RESULT 1
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Rilebner, P.J. submitted to the EMBL Data Library, August 1994
A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T A;Reference number: S47355
A;Accession: S47400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rinkano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restx
A;Reference number: PT0209; MUID:91217621; PMID:1902501
A;Accession: PT0217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompat A;Reference number: PH1430; MUID:93171821; PMID:8436911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47400
                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z35678; NID:g527535; PIDN:CAA84747.1; PID:g527536
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                          Gaps
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Score 28; DB 2; Length 12;
Pred. No. 1.2e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                             T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
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Pred. No. 1.2e+02;
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Best Local Similarity 41.7%;
Matches 5; Conservative
           38.9%;
62.5%;
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71.4%;
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           Query Match 38.9
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
                                                                                                                                                                                                                     1 CASSLGNT
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A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
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C;Species: Mus musculus (house mouse)
C;Species: IO-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1463
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko J. Exp. Med. 177, 811-820, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell receptor beta chain (clone Cw3/Ag, Cw3/Cas1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C;Accession: S26549; S26550
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid A;Title: Mad. 176, 439-447, 1992
A;Title: H-2-restricted cytolyvic T lymphocytes specific for HLA display T cell receptor A;Reference number: S26512; MUID:92364546; PMID:1380061
                                                                                         C, Accession: 847357

R, Lehmer, P. J.

By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By Lehmer, By 
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           T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
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A,Residues: 1-12 <CA2>
A,Cross-references: BMBL:X68000
A,Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A;Accession: S26550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29.5; DB 2;
Pred. No. 68;
2; Mismatches 1;
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A; Residues: 1-12 < CAS>
A; Residues: 1-12 < CAS>
CS. Saperimental source: cytolytic T-lymphocyte
C; Superfamily: immunoglobulin homology
C; Keywords: receptor; T-cell
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Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity
Matches 5; Conserv
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A; Residues: 1-12 < CAS>
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T-cell antigen receptor VJ junction beta chain - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-dan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47395
R;Lehner, P.J.
R;Lehner, P.J.
A;Description: Human HIA-A0201 restricted recognition of influenza A is dominated by T A;Reference number: S47355
A;Accession: S47395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rilehner, P.J. submitted to the EMBL Data Library, August 1994 submitted to the EMBL Data Library, August 1994 A; Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T A; Reference number: 847355
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C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47381
                      A;Accession: S57575
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1.11 <BUR>
A;Cros-references: EMBL:Z49953; NID:g887510; PIDN:CAA90224.1; PID:g887511
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Wolecule type: mRNA
A;Residues: 1-12 <LEA
A;Cross-references: BMBL:235715; NID:9527525; PIDN:CAA84784.1; PID:9527526
C;Keywords: T-cell receptor
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35698; NID:g527487; PIDN:CAA84767.1; PID:g527488
C;Keywords: T-cell receptor
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Pred. No. 2.9e+02;
1; Mismatches 6; Indels
                                                                                                                                                                                          36.1%; Score 26; DB 2; Length 11; 71.4%; Pred. No. 2.5e+02; ative 1; Mismatches 1; Indels
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T-cell antigen receptor VJ junction beta chain - human
C,Species: Homo sapiens (man)
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ilarity 41.7%;
Conservative
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Best Local Similarity 71.49
Matches 5, Conservative
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  A;Reference number: S57494
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Best Local Similarity
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Best Local Similarity
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R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: S47391
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 1-12 <LEH>
A;Cross-references: EMBL:Z35712; NID:g527519; PIDN:CAA84781.1; PID:g527520; EMBL:Z35701;
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribehner, P.J.
submitted to the EMBL Data Library, August 1994
A; Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T of A; Reference number: S47355
A; Accession: S47383
                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Lehner, P.J.
submitred to the EMBL Data Library, August 1994
submitred to the EMBL Data Library, August 1994
A; Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A; Reference number: 847355
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C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                     T-cell antigen receptor VJ junction beta chain - human C;5pecies: Homo saplems (man)
C;5pecies: Homo saplems (man)
C;5pec: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: 547391; 547386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell antigen receptor VJ junction beta chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35709; NID:g527513; PIDN:CAA84778.1; PID:g527514
C;Keywords: T-cell receptor
                                                                                                                      Gaps
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                                                                      Score 27; DB 2; Length 11; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27; DB 2; Length 12;
Pred. No. 1.8e+02;
0; Mismatches 6; Indels
                                                                                                                    1; Indels
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Best Local Similarity 62.53
Matches 5; Conservative
                                                                                                                      5; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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A;Residues: 1-11 <NAK>
C;Keywords: T-cell receptor
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C;Accession: S2371
R;Pluschke, G; Ricken, G; Taube, H; Kroninger, S.; Melchers, I.; Peter, H.H.; Bichman B:Pluschke, G; Ricken, G; Taube, H; Kroninger, S.; Melchers, I.; Peter, H.H.; Bichman A;Title: Biased T cell receptor, V(alpha) region repertoire in the synovial fluid of rheu A;Reference number: S23364; MUID:92037820; PMID:1657615
A;Accession: S23371
A;Accession: S23371
A;Molecule type: mRNA
A;Residues: 1-10 < PLU>
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S47382; S47370
R;Lehner, P.J.
B;Lehner, P.J.
By Description: Human HiA-A0201 restricted recognition of influenza A is dominated by T of A;Reference number: S47385
A;Reference number: S47385
A;Accession: S47382
A;Accession: S47382
A;Accession: S47383
A;Accession: Braininary
A;Molecule type: MRNA
A;Molecule type: MRNA
A;Residues: 1-13 < LEBA
A;Cross-references: EMBL:Z35687; NID:g527463; PIDN:CAA84756.1; PID:g527464; EMBL:Z35695; C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor alpha chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X58166
C;Keywords: T-cell receptor
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1 CASSM-RSTDT 10
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2 SGEAGKST 9
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S23371
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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March 8, 2004, 11:48:53; Search time 11 Seconds
(without alignments)
61.537 Million cell updates/sec protein search, using sw model 1 CASELGKSTNTFC 13 US-09-761-636A-5 72 Perfect score: OM protein Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

597 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 13

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Query Result

-	No.	Score	Match	Match Length DB	80	ai.	Description
	-	23	31.9	12	m	PSP3 PHYPA	P80662 physcomitre
	7	20	27.8	12	7	V23K WSSV	
	e	20	27.8	13	Н	LIGA_TRAVE	
	4	20	27.8	13	Н	PSBP PINPS	P81668 pinus pinas
	Ŋ	13	26.4	10	П	COXM_RAT	
	9	18	25.0	12	ч	UR2B_CATCO	P04559 catostomus
	7	18	25.0	13	-	FARB ASCSU	
	80	17	23.6	12	⊣	UR2B_CYPCA	
	6	16	22.2	σ'n	Н	XYLA STRSQ	
	10	16	22.2	11	Н	TKC2_CALVO	P41518 calliphora
	11	16	22.2	12	Н	CXL3_CONMR	
	12	16	22.2	12	Н	TA10 TREME	P01371 tremella me
	13	16	22.2	13	Н	CXAA_CONST	P28878 conus stria
	14	16	22.2	13	н	HPB9_RANES	P32416 rana escule
	15	15	20.8	o,	-	CCAP_CARMA	P38556 carcinus ma
	16	15	20.8	σ	Н	FARS ASCSU	
	17	15	20.8	σ	П	SAMP_MUSCA	P19095 mustelus ca
	18	15	20.8	σ,	П	SAP STOVA	
	19	15		10	Н	COXQ RABIT	P80336 oryctolagus
	20	15	20.8	10	٦	ODP2_BOVIN	
	21	15	20.8	11	7	CX5A_CONAL	P58848 conus aulic
	22	12	20.8	11	Н	CX5B CONAL	
	23	15	20.8	11	Н	FAR9 CALVO	
	24	15	0	11	٦		P82651 hoplobatrac
	25	15	20.8	12	Н	CXA1 CONIM	P50983 conus imper
	56	15	20.8	12	Н	NO40 LOTJA	022426 lotus japon
	27	15	20.8		Н	SOIS_BACSU	P80863 bacillus su
	28	15	20.8	13	Н	CRBL_VESTR	P17231 vespa tropi
	53	15	20.8	13	Н	CXA2 CONGE	conns
	30	15	20.8		Н	GER1_HORVU	P28525 hordeum vul
	31	15	20.8		Н	GER2_HORVU	
	32	14	19.4		Н	IGAO_DACDE	P06294 dactylium d
	33	14	19.4	7	Н	UC24_MAIZE	P80630 zea mays (m

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Gaps

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similarity 57.1%; Pred. No. 3.2e+02; Af. Conservative 1; Mismatches 2; Indels

Query Match Best Local Similarity Matches 4; Conserv

6 GKSTNTF 12

3 GESANVF 9

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RESULT 2

VAJK WSSV

1D VAJK WSSV

AC P82005.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 23 kDa structural polyprotein (Fragment).

OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.

OX NCBL TaxID=92652;

RN |1]

RP SEQUENCE.

RC STRAINE=SOUth Carolina;

RC STRAINE=SO14217; PubMed=10752552;

RA Mang Q., Poulos B.I., Lightner D.V.;

P83281 macrobrachi P41488 locusta mig Q46464 campylobact P30350 locusta mig P19851 gallus gall P28600 oncorhynchu P20690 rana catesb P32080 homo sapten P81022 polyodon sp P17332 vespa manda P80747 bos taurus		d) equence update) tent 2 (OEE2) (24 kDa subunit of oxygen ten II) (Fragment). reptophyta; Embryophyta; Bryophyta; iales; Funariaceae; Physcomitrella88ki R.; and plastome-encoded energy-converting d in the regulation of photosystem II. lloroplast thylakoid membrane; associated complex. the pabp family. II; Chloroplast; Thylakoid; Membrane; BD2B0D54D7C44DC5 CRC64;
1 FAR8 MACRS 1 LPK2 LOCMI 1 SYK_CAMUP 1 TKL4 LOCMI 1 TKNB_CHICK 1 TKNB_CHICK 1 TKNC_RANCA 1 TKNC_RANCA 1 URA6 BACSU 1 UR2 POLSP 1 UR2 FOLSP 1 CRBL VESWA 1 ITBS_BOVIN	GNMENTS	PROGEZ: 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Created) 01-0CT-2096 (Rel. 34, Last amortation update) 01-0CT-2096 (Rel. 40, Last amortation update) 001-0CT-2001 (Rel. 40, Last amortation update) 00xygen-evolving enhancer protein 2 (OBE2) (24 kDa subunit of ox evolving system of photosystem II) (Fragment). Bryopabida: Punariales (Ross). Bryopabida: Funariales; Funariaceae; Physcomitrella. NCBI TaxID=3218; [1] 12 TaxID=3218; [1] 13 Expubmed. 14 Rastem B., Buck F., Nuske J., Reski R.; MEDLINE=97275459; PubMed=9129336; MESASTEM B., Buck F., Nuske J., Reski R.; MEDLINE=97275459; PubMed=9129336; MESASTEM B., Buck F., Nuske J., Reski R.; FOYCHINIA AND NOTION: Chloroplast thylakoid membrane; associated the photosystem II complex. -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated the photosystem II; Chloroplast; Thylakoid; Membran Miltigene family. -1- SIMILARITY: Belongs to the pabp family.
19.4 19.4 18.1 18.1 18.1 18.1 18.1 18.1 18.1 18		PEOS-FILIA SIANDARD, FILE PEOS-FILEA SIANDARD, 01-OCT-1996 (Rel. 34, Last sequency 01-OCT-2000 (Rel. 34, Last sequency 01-OCT-2001 (Rel. 40, Last sequency 05-COT-2001 (Rel. 4
44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	SUL	DT 0-0CT-1996 (Rel. DT 01-0CT-1996 (Rel. DT 10-0CT-1996 (Rel. DE 0X) DT 16-0CT-2001 (Rel. DE 0X) DE 0X) DE 0X DE 0

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Eur. J. Biochem. 230:235-241(1995).
-!- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Wistar; TISSUR-Liver;
MEDLINE-95324529; PubMed=7601105;
Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
"Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.";
                                                                                                                                                                     Electrophoresis 20:1098-1108(1999).
-!- FUNCTION: May be involved in the regulation of photosystem II.
-!- FUNCTION: May be involved in the regulation of photosystem II.
-!- SUBCELLULAN LOCATION: Chloroplast thylakoid membrane; associated with the photosystem II complex (By similarity).
-!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein (spot NI79) is: 5.9, its MW is: 22 kDa.
-!- SIMILARITY: Belongs to the pabp family.
-- Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
NON TER 13 13
-- SEQÜENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                      MEDLINE=99274088; PubMed=10344291;
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Prigerio J.-M., Plomion C.,
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cytcohrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus.
NCBL_TaxID=71647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.4%; Score 19; DB 1; Length 10; 66.7%; Pred. No. 1.5e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                           27.8%; Score 20; DB 1; Length 13; 42.9%; Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI TaxID=10116;
                                                                        rissum=Needle;
                                                                                                                                                           proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragment).
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SEQUENCE
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-1- PATHARY: Lignin degradation; first step.
-1- SIMILANITY: Belongs to the peroxidase family. Ligninase subfamily. PIL 5.04013; S04013.

InterPro; IPR002016; Peroxidase.
InterPro; IPR002016; Peroxidase.
PROSITE: PS00435; PEROXIDASE 1; PRATIAL.
PROSITE: PS00436; PEROXIDASE 2; PRATIAL.
Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein; Non Ligene family; Lignin degradation.
NON IER.
SEQÜENCE 13 AA; 1299 MW; 22C50ED5872A4338 CRC64;
        "Protein analysis of geographic isolates of shrimp white spot syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 247:143-146(1989).
-!- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-
C(beta) cleavage of the propyl side chains of lignin.
-!- CATALYMIC ACTIVITY: 1,2-bis(3, 4-dimethoxyphenyl)propane-1,3-diol +
H(2)O(2) = veratraldehyde + 1-(3,4-dimethylphenyl)ethane-1,2-diol
                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Oxygen-evolving enhancer protein 2 (OBE2) (23 kDa subunit of oxygen evolving system of photosystem II) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                              Trametes versicolor (White-rot fungus).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Aphyllophorales; Trametes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pinus pinaster (Maritime pine).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
"Trametes versicolor ligninase: isozyme sequence homology and
substrate specificity.";
                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last annotation update)
Ligninase A (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.8%; Score 20; DB 1; Length 13; 66.7%; Pred. No. 1.2e+03;
                                                                                                                           Length 12;
                                                                                                                                                           3; Indels
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                                                                                          12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;
                                     Arch. Virol. 145:263-274(2000).
-!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
NON TER
                                                                                                                        Score 20; DB 1; I
Pred. No. 1.2e+03;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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MEDLINE-89211432; Pubmed=2707445;
                                                                                                                                                                                                                                                                                                                                             (Rel. 17, Created)
(Rel. 17, Last seq
                                                                                                                           27.8%;
57.1%;
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                                                                                                                                         Local Similarity 57.1
nes 4; Conservative
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Matches 4; Conserv
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6 GKNTAT 11
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28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                    peroxidase)
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ID _LIGA_TRAVE
                                                                                          SEQUENCE
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PSBP PINPS
                            virus.'
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HAMAP; MF 00455; -; 1.
InterPro; IPR001998; Xylose isom.
PROSITE; PS00172; XYLOSE ISOMERASE 1; PARTIAL.
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                                                                                                  STANDARD;
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Best Local Similarity
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                                                                                              UR2B CYPCA
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                                                                                                                                P04561;
                                                                UR2B_CYPCA
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                                                                                                  STTWN PROCESS TO THE PROPERTY OF STATE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides 4:367-373(1983).

-!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory system. It has a suggested role in osmoregulation and as a corticortrophin-releasing factor.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the urotensin 2 family.

PIR: JS0424; JS0424.

InterPro: IPR001483; Urotensin II.

Pfam; PF02083; Urotensin II.

PROSITE; PS00984; UROTENSIN II: 1.
                                                  13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Urotensin IIB (U-IIB) (UIIB).
Catostomus commersoni (White sucker).
Rikazyota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Catostomidae; Catostomus.
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Eukaryota, Metazoa, Nematoda; Chromadorea, Ascaridida; Ascaridoidea;
Ascarididae; Ascaris.
NCBI_TaxID=6253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    McMaster D., Lederis K.; "Isolation and amino acid sequence of two urotensin II peptides from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18; DB 1; Length 13;
Pred. No. 2.9e+03;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 11
12 AA; 1437 MW; 73961BDBBB79CBBB CRC64;
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9CAEC650D6886B05 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
FWRFamide-like neuropeptide AFII.
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12 AA.
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PRT;
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MEDLINE=95380362; PubMed=7651904;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=84041959; PubMed=6138758;
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Neuropeptide, Amidation.
MOD RES 13
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides 4:367-373 (1983)
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2 SNTEC 6
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DISULFID
SEQUENCE
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Matches
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Munckata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;

(In) Rich D.H., Gross E. (eds.);

(In) Rich D.H., Gross E. (eds.);

Proceedings of the 7th American peptide symposium, pp.69-72,

Pierce Chemical Co., Rockford II. (1981).

-!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory system. It has a suggested role in osmoregulation and as a corticotropin-releasing factor.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SUBCATION: DROUGHS; Urotensin II.

PEAM: PRO2083; Urotensin II.; I.

PROSITE; PS00984; UROTENSIN II; I.
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Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
"Purification and characterisation of glucose (xylose) isomerase from Chainia sp. (KC. 182-5-1)."
Biochem. Biophys. Res. Commun. 155:411-417 (1988).
-i- FUNCTION: Involved in D-xylose catabolism.
-i- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
                                       10-CTT-2013 (Rel. 05, Last sequence update)
10-CTT-2013 (Rel. 42, Last amotation update)
Urotensin II-beta (UII-beta) (U-II-beta).
Cyprinus carpio (Common carp).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygi; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprindae; Cyprinus.
NCBI_TAXID=7962;
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-i- SUBUNIT: Homoretramer.
-i- SUBULILIAR LOCATION: Cytoplasmic.
-i- SIMILARIY: Belongs to the xylose isomerase family.
PIR; A31576; A31576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces sp. (atrain NCL 82-5-1).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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73960A9FB879CEBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17; DB 1; I Pred. No. 4.1e+03;
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01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last amoutation update)
Xylose isomerase (EC 5.3.1.5) (Fragment).
12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA.
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venom of Conus marmoreus.";
J. Biol. Chem. 275:39516-39522 (2000).

-i. FUNCTION: Inhibits the neuronal noradrenaline transporter.
-i. SUBCELLULAR LOCATION: Secreted.
-i. TISSUE SPECIFICITY: Expressed by the venom duct.
-i. MASS SPECIFOMETRY: NW-1262.77; NW ERR=0.07; METHOD=Electrospray.
-i. MSAS SPECIFOMETRY: Ms-1262.77; NW ERR=0.07; METHOD=Electrospray.
-i. SIMILARITY: Belongs to the chi/lambda-conotoxin family.
                                                                                                                                                                                                                                                                                                        HYDROXYLATION.
277AAE2422D5A2C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                22.28;
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Matches 2; Conservative
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TISSUE=Venom;
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CXAA_CONST
1D CXAA_CONST
AC P28878;
DT 01-DEC-1992
DT 28-FEB-2003
DE Albha-contco
C Abogastropod
C Abogastropod
C Neogastropod
C Ne
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P01371;
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SEQUENCE
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Best Local S
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TA40_T
AC 901371
DT 21-JUL
DT 21-JU
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
Calliphoridae; Calliphora.
NCBL_TaxID=27454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macasur D.A.Y.

"Callitachykinin I and II, two novel myotropic peptides isolated from the blowfly, Calliphora vomitoria, that have resemblances to tachykinins.";
Peptides 15:761-768(1994).
-!- FUNCTION: Myoactive peptide.
-!- SIDELELULAR LOCATION: Secreted.
-!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
--- Tachykinin; Neuropeptide; Amidation...
      PROSITE; PSO0173; XYLOSE_ISOMERASE_2; PARTIAL.
ISOMERABE; PER Shunt; Xylose metabolism; Metal-binding; Magnesium.
NON TER 9 A8; 983 WW; F64BAIEDCSB87DDI CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, AND SYNTHESIS.
MEDLINE-95075727; PubMed=7984492;
Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
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                                                                                                                                                                                                                      Gaps
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Bukaryota; Metazoa; Molluedas; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 16; DB 1; Length 11;
Pred. No. 5.7e+03;
0; Mismatches 4; Indels
                                                                                                                                                    22.2%; Score 16; DB 1; Length 9; 60.0%; Pred. No. 1.4e+05; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
15D7E3F9C9CDD444 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Callitachykinin II.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calliphora vomitoria (Blue blowfly).
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11 AA; 1103 MW;
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Best Local Similarity 42.3%,
                                                                                                                                                                                                                   3; Conservative
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                                                                                                                                                                                Local Similarity
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SAHTF 9
                                                                                                                                                                                                                                                                           8 STNTF 12
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P41518;
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-i-FUNCTION: Tremerogen A-10 is produced by the a mating-type cells and induces formation of conjugation tubes in a mating-type cells. PIR A01642; UJUGO.
Lipporotein; Prenylation; Methylation; Pheromone.
Lipto 12 12 S-12-hydroxyfarnesyl cysteine.
MOD RES 12 METHYLATION: METHYLATION: SEQUENCE 12 AA; 1246 MM; 84EF574959676DCS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tremellă mesenterica (Jelly fungus).
Eukaryota, Fungi, Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetides, Tremellales; Tremellaceae; Tremella.
WCBI_TaxID=5217;
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                                                                     Gape
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Neogastropoda; Concidea; Conidae; Conus.
NCBI_TaxID=6493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sakagami Y., Yoshida M., Isogai A., Suzuki A.; "Peptide sex hormones inducing conjugation tube formation in compatible mating-type cells of Tremella mesenterica."; Science 212:1525-1527(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alpha-conoloxin SIA (SIA).
Conus striatus (Striated cone).
Bukaryota; Metazoa; Mollusca; Gastropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%; Score 16; DB 1; Length 12; 50.0%; Pred. No. 6.2e+03; ive 1; Mismatches 1; Indels
Score 16; DB 1; Length 12; Pred. No. 6.2e+03;
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Job time : 11 secs
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                                                                                 inhibit them.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification and characterization of bioactive peptides from skin
                             'Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2093 (Rel. 42, Last annotation update)
Hemolytic protein B9 (Fragment).
Eana esculenta (Edible frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annura; Neobatrachia; Ranoidea; Ranidae; Rana.
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                                                Biochemistry 30:9370-9377(1991).
-1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, bind to the nicotinic acetylcholine receptors (nAChR) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90198965; PubMed=2317508;
Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
Barra D., Bossa F.;
    Wyers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J., Olivera B.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.2%; Score 16; DB 1; Length 13; 66.7%; Pred. No. 6.7e+03; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                         Score 16; DB 1; Length 13;
Pred. No. 6.7e+03;
1; Mismatches 4; Indels
                                                                                                                                                                                          AMIDATION.
DEF1931982457EBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AA; 1402 MW; C6B41A765DF9287D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amphibian defense peptide; Amidation; Hemolysis.
                                                                                                                              PIR; A40312; NTKNAS.
POSt$/A70aptic neurotoxin; Neurotoxin; Toxin;
Acetylcholine receptor inhibitor; Amidation.
                                                                                                                                                                                                                                                                                                                                             13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               extracts of Rana esculenta.";
Biochim. Biophys. Acta 1033:318-323(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Shows hemolytic activity.
-!- SUBCELLUIAR LOCATION: Secreted.
-- TISSUE SPECIFICITY: Skin.
PIR: S09019; S09019.
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MEDLINE=91369955; PubMed=1892838;
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13 AA; 1461 MW;
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                                                                                                                                                                                                                                              3; Conservative
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Best Local Similarity
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ID CCAP CARMA
AC P38556;
                                          receptors.";
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SEQUENCE
                                                                                                                                                                               DISULFID
MOD RES
SEQUENCE
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Furtury K., Linds S., Reynolds S.E., Ota R.B., Hackett M., Schooley D.A., Schooley D.A., Isolation and identification of a cardioactive peptide from Tenebrio molitor and Spodoptera eridania.", Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).

-i - FUNCTION: The effect of CQAP is both ino- and chronotropic.
-i - SURCELAULAR LOCATION: Secreted.
-i - TISSUE, SPECIFICITY: Stored in pericardial organs and released
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SPECIES-C.maenas, TISSUE-Pericardial organs;
Stangier J., Hilbich C., Beyreuther K., Keller R.;
Stangier J., Hilbich C., Beyreuther K., Keller R.;
"Unusual cardioactive peptide (CCAP) from pericardial organs of the shore crab Carcinus maenas.";
Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES=M.sexta;
MEDLINE=9305024;
MEDLINE=9305024;
Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
"Primary structure of a cardioactive neuropeptide from the tobacco
01-OCT-1994 (Rel. 30, Created)
[01-OCT-1994 (Rel. 30, Last sequence update)
[15-MAR-2004 (Rel. 30, Last sequence update)
[15-MAR-2004 (Rel. 43, Last annotation update)
[16-MAR-2004 (Rel. 43, Last annotation update)
[17-MAR-2004 (Rel. 43, Last annotation update)
[18-MAR-2004 (Rel. 43, Last annotation update)
[18-MAR-2004 (Rel. 43, Last annotation update)
[18-MAR-2004 (Rel. 43, MAR-2004 (Rel. 43, Malacostraca, Malacostraca, Buaracotataca, Bucarida, Decapoda, Pleocyemata, Brachyura, Eumbrachyura, Portunoidea, Portunidae, Carcinus.
[18-MAR-2004 (Rel. 43, MAR-2004 (Rel. 43, MAR-2004)]
[18-MAR-2004 (Rel. 43, MAR-2004
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9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;
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MEDLINE=94176032; PubMed=8129851;
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sp_archeap:*

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MEDILINE-92011443; PubMed=1931944;

MEDILINE-92011443; PubMed=1931944;

MEDILINE-92011443; PubMed=1931944;

Mediand T.E., Yount R.G.;

"Direct photoaffinity labeling of gizzard myosin with vanadate-trapped adenosine diphosphate.";

adenosine diphosphate.";

Biochemistry 30:1015-10132(1991).

PIR: A23695; A23695.

NON_TER
             Myosin (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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MEDLINE-83017896; PubMed=6927854;
Anccard J.B., Chmelo R., Pickup D.J., Joklik W.K.;
"Sequences a both termini of the 10 genes of reovirus serotype 3
(strain Dearing).";
Virology 121:307-319(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDIATE 123853; MEDIATE-8917877; PubMed-7123853; MEDIATE-8171877; J. J.K., Keene J.D., Joklik W.K.; "The sequences at the termini of four genes of the three reovirus
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01-NOV-1996 (TERMBLRel. 01, Last sequence update)
01-NOV-1996 (TERMBLRel. 19, Last annotation update)
Reovirus serotype 3 N3 (Fragment).
Reovirus (type 3 / strain Dearing).
Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
NCBI_TAXID=10886;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Virology 121:320-326(1982).
EMBL; J02323; AAA47259.1; -.
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Local Similarity 55.6%;
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STRAIN=HPW16E2CC7;
WattB K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human Papillomavirus type 16
"Sequence variation and physical state of human Papillomavirus type 16
"Servical cancer isolates from Australia and New Caledonia.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF407220; AALO1406.1;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
NCBI_TaxID=10581;
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-DEC-2001 (TERMBLrel. 19, Last sequence update)
01-DEC-2001 (TERMBLrel. 19, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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                                              13 AA.
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                                              PRELIMINARY;
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                                                                                                                             El protein (Fragment).
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NCBI_TaxID=10581;
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SEQUENCE
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SEQUENCE
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                                                                Q918T4;
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Matches

RESULT 3

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Best Loc Matches

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RESULT 4
Q9PS67
ID Q9PS1
AC Q9PS1
DT 01-M

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Cryptococcus neoformans var. neoformans.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
[1]
                                                                                                                                                                                                                                                                                                                                                          Gaps
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Plant Cell 11:971-986(1999).
EMBL, Y18256; CAB41875.1; -.
SEQÜENCE 11 AA, 1035 MW; CD3806DDA8772AAD CRC64;
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MEDLINE-99264316; PubMed=10330480;
Cabrillac D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
Dumas C., Gaude T., Cock J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                              Goraya J., Knoop F.C., Conlon J.M.;
"Ranatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, Rana catesbelana.",
slochem. Blophys. Res. Commun. 250:189-592(1998).
-i- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
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Pred. No. 5e+03;
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Pred. No. 6.5e+03;
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Last annotation update)
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Last annotation update)
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-!- SUBCELLULAR LOCATION: SECRETED.
GO; GO:0006805; P:xenobiotic metabolism; IEA.
Antibiotic.
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                                         TISSUE=SKIN;
MEDLINE=98422096; PubMed=9751476;
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50.0%;
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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Guery Match
Best Local Similarity 50.00,
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                                                                                                                                                       Nonneman D., Geesink G.H., Koohmaraie M.;
"Differential splicing and protein isoforms of ovine calpastatin.";
Submitred (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF192536; AAG31681.1;
EMBL; AF192535; AAG31687.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goraya J., Khoop F.C., Conlon J.M.;
"Ranatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, Rana catesbelana.";
Blochem. Blophys. Res. Commun. 250:589-52(1998).
-:- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
                   Ovis aries (Sheep).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBI_TaxID=8400;
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia: Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBI_TaxID=8400;
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Pred. No. 5e+03;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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GO; GO:0006805; P:xenobiotic metabolism; IEA.
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01-JUN-2003 (TrEMBLrel. 24, Last anno
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80.0%;
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Calpastatin (Fragment).
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Best Local Similarity
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SEQUENCE.
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Herve D., Rogard M., Levi-Strauss M.; "Molecular analysis of the multiple Golf alpha subunit mRNAs in the
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Goraya J., Knoop F.C., Conlon J.M.;
"Ramatuerins: antimicrobial peptides isolated from the skin of the American bullfrog, Rana catesbeiana.";
Blochem. Blophys. Res. Commun. 250:589-592(1998).
-!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBL_TaxID=8400;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNA-1903 (TrEMBLrel. 24, Last amoniation update)
N-acetylglucosamine (Betal-4) galactosyl transferase (EC 2.4.1.90)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Pred. No. 7.7e+03;
0; Mismatches 1; Indels
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                                                                                                                                                                              27.8%; Score 20; DB 11; Length 13 57.1%; Pred. No. 7.78+03; Live 1; Mismatches 2; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
RANATUERIN 8.
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-- SUBCELLULAR LOCATION: SECRETED.
GO; GO:0006805; P:xenobiotic metabolism; IEA.
Antibiotic.
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                                        rat brain.";
Brain Res: Mol. Brain Res; 32:125-134(1995)
BMB1; 880330; AAP32222.1;
NON TER 13
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                                                                                                                                    13 AA; 1312 MW;
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Matches 5; Conservative
                                                                                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  4 LGNSSKT 10
                                                                                                                                                                                                                                                                        5 LGKSTNT 11
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                                                                                                                                      SEQUENCE
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Q61331
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                            Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                    Carter D.A., "Presence of alpha and a mating types in environmental and clinical collections of Cryptococcus neoformans var. gattii strains from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88422096; PubMed=9751476;
Goraya J., Knoop F.C., Conlon J.M.;
"Ranatuerinas antimicrobial peptides isolated from the skin of the American bullfrog, Rana catesbelana.";
Blochem. Blophys. Res. Commun. 250:589-592(1998).
-- SUBCELLUIAR LOCATION. SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANATUERIN 5.
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
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SEQUENCE FROM N.A.
STRAIN-EBS884, BAL 3, and CBS6989;
MEDLINE-99380307; PubMed=10449476;
Halliday C.L., Bui T., Krockenberger M., Malik R., Ellis D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DB 13; Length 12;
Pred. No. 7.1e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                        1 27.8%; Score 20; DB 3; Length 12; Similarity 100.0%; Pred. No. 7.1e+03; 3; Conservative 0; Mismatches 0; Indels
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12 AA; 1307 MW; 5AF9B485D5A735B7 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
G<ALPHANOLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                    Australia.";
J. Clin. Microbiol. 37:2920-2926(1999).
EMBL, AFISS349; AAF20374.1; -.
EMBL; AFISS349; AAF20372.1; -.
EMBL; AFISS348; AAF20373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Dest Local Similarity 83.3",
Est Local Similarity 63.3",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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EMBL; D00315; BAA00217.1; -.
GO; GO:0003945; F:N-acetyllactosamine synthase activity; IEA.
GO; GO:0016757; F:transferase activity, transferring glycosyl. . ; IEA.
Glycosyltransferase; Transferase.
NON TER 1 1 1
NON_TER 12 12
SEQÜENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol-JUN-1998 (TrEMBLrel. 06, Created)
Ol-JUN-1998 (TrEMBLrel. 06, Last sequence update)
Ol-JUN-1998 (TrEMBLrel. 19, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Prolactin (Fragment).
Whs musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Musc.
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12 AA; 1283 MW; 304EA40668387728 CRC64;
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3 SSGLGKT 9
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054809
AC 05480
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Search completed: March 8, 2004, 11:55:23 Job time : 40 secs

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March B, 2004, 11:48:18 ; Search time 53 Seconds
(without alignments)
69.304 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                  1586107 seqs, 282547505 residues
                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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72
1 CASELGKSTNTFC 13
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Perfect score:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseg 29Jan04:*	geneseqp1980s:*	geneseqp1990s:*	geneseqp2000s:*	geneseqp2001s:*	geneseqp2002s:*	geneseqp2003as:*	geneseqp2003bs:*	general months : *
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Database								

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	TOTAL TOTAL	Aau04524 VEGF base	VEGE	VEGF	VEGF	VEC	Felin	Immi	_	Ξ		Imminut	_							_			Human	700		
SUMMARIES	ID		AAU04524	AAU04534	AAU04535	AAU04537	AAU04536	AAY57039	ABJ04094	AAY66781	AAB75626	AAY66787	ABJ04095	AAY48678	AAB10896	AAE26783	AAB10895	ABJ04091	ABJ04088	ABJ04570	AAW42705	AAM43317	AAW34877	AAW34865	AAU28829	AAU26477	ABG67372
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ď	Query Match		100.0	95.8	90.3	90.3	84.7	44.4	44.4	41.7	40.3	40.3	40.3	38.9	38.9	38.9	38.9	38.9	38.9	•		37.5	37.5	37.5	37.5	37.5	37.5
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Ada23476 Alzheimer	Aab26567 Human IGE	Aau16900 Peptide #	Abi00485 Human IGE								SCP-1	Human						_	Epitop
6 ADA23476	3 AAB26567	4 AAU16900	5 ABJ00485	5 ABJ04090	5 ABJ04092	5 ABJ04093	4 AAU08458	2 AAW83264	2 AAW67159	2 AAW97980	3 AAY76718	6 ABP74688	7 ADC09547	4 AAG84316	4 AAG96997	4 AAG96549	5 ABP47552	6 ABP74689	7 ADC09548
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26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAU ID	RESULT 1 AAU04524 LD AAU04524 Btandard; peptide; 13 AA.
\$ \$ \$	AAU04524;
1	26-SEP-2001 (first entry)
2日3	VEGF based monocyclic peptide 1.
	Human; VBGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
\$ 8 F	Synthetic.
	<pre>Key Disulfide-bond 113 /note= "This bond cyclises the peptide"</pre>
18	WO200152875-A1.
(日)	26-סטו-2001.
₹ £ \$	18-JAN-2001, 2001WO-US001533.
EEE	18-JAN-2000, 2000US-0176293P. 16-MAX-2000, 2000US-0204590P.
1	(LUDW-) LUDWIG INST CANCER RES.
1	Achen MG, Hughes RA, Stacker S, Cendron A;
1 83	WPI; 2001-442248/47.
\$ # # # # # # # # # # # # # # # # # # #	Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.
S 25	Claim 49; Page 32; 102pp; English.
ខម	
ខនន	VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocylic peptide by a measuring betabet acarbon separation distances on opposite antibarallel strands of a
	S TO ASSESSED THE PROPERTY OF

Example 25; Page 47; 102pp; English.

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic cyclising the peptides of comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis.

Comeovacularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or lymphangiogenesis.

Compandition is diabetic retinopathy, psoriasis, arthropathy, recondition is diabetic retinopathy, psoriasis, arthropathy, cerebrovascular accident, post-engosis, head, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive companding angiogenesis and angiogenesis and angiogenesis are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in pertipheral limbs or in lungs, peritoneal cavity, pleura, or brain. The peptides are used to image blood vessels and lymphatic cor brain. The peptides are used to image blood vessels and lymphatic cor brain. The peptides are used to image blood vessels and lymphatic corrections inflammation with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and also existed and also best inflammation, especially rheumatoid arthritis, psoriasis and also existed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13;
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100.0%; Pred. No. 2.1e-05;
ive 0; Mismatches 0; Indels

    .13
/note= "This bond cyclises the peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU04534 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF based monocyclic peptide 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 13; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2000; 2000US-0176293P, 16-MAY-2000; 2000US-0204590P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200152875-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04534;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Achen MG,
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c to cyclisation are used to interfere with angiogenesis,

neovascularisation or lymphangiogenesis in a mammal with a condition

characterised by angiogenesis in a mammal with a condition

characterised by angiogenesis in covascularisation or lymphangiogenesis.

The condition is diabetic retinopathy, psoriasis, arthropathy,

the angiona, vascularised malignant or benign tumour, post-recovery

crebrovascular accident, post-angioplasty restenosis, head, heat or cold

traum, substance-induced neovascularisation of the liver, excessive

creabrovascular accident, post-angioplasty restenosis, head, heat or cold

traum, substance-induced neovascularisation of the liver, excessive

creaple hypertension induced neovascular sequelae, or chronic liver

infection. The peptides are also used to modulate vascular permeability

crimfection in peripheral limbs or in lungs, peritoneal cavity, pleura,

or brain. The peptides are used to image blood vessels and lymphatic

crobing the monomeric and bicyclic peptides are used to interfere

crownulation or biological activity induced by VEGF, VEGF-C or -D and

are also used in combination with an anti-inflammatory agent, to treat a

chronic inflammation, especially theumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                           whose 3-dimensional structure is modelled on the expose loop of human VEGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betacathon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amino acid deleted prior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; VEGF; vascular endothelial growth factor; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neovascularisation, lymphangiogenesis, psoriasis, tumour;
diabetes induced neovascular sequelae, rheumatoid arthritis;
diabetic retinopathy; chronic inflammation, cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels

    13 "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB 4; I
Pred. No. 6.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU04535 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEGF based monocyclic peptide 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JAN-2001; 2001WO-US001533.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CATELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200152875-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU04535;
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of by a measuring beta carbon separation distances on opposite antiparallel strands of a complete of producing a monomeric monocyclic peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides, and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with amplogenesis, neovascularisation or lymphanjogenesis in a mammal with a condition is diabetic retinopathy, psortassis, arthropathy, characterised by angiogenesis, neovascularisation or lymphanjogenesis. The condition is diabetic retinopathy, psortassis, head, heat or cold crander substance and maintain to benign tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold cormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver cormulation in peripheral limbs or in lungs, peritoneal cavity, pleura, cormulation in peripheral limbs or in lungs, peritoneal cavity, pleura, cormulation in peripheral limbs or in lungs, peritoneal cavity, pleura, vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF. Cormic inflammation, especially rheumatoid arthritis, psoriasis and chabetic retinopathy.
                                                                                                                     Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 65; DB 4; Length 13;
Pred. No. 0.00033;
2; Mismatches 0; Indels

    .13
/note= "This bond cyclises the peptide"

                                            Cendron A;
                                                                                                                                                                                                                        Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                            Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU04537 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGF based monocyclic peptide 15.
(LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||||
| CASELGKTSNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CASELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
                                         Hughes RA,
                                                                                 WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
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                                         Achen MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU04537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human CC whose 3-dimensional structure is modelled on the expose loop of human CC Wascular endothelial growth factor. The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betactor producing a monomeric monocyclic peptide by producing a monomeric monocyclic peptides, dimeric bicyclic peptides loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis,

CC peptides and a cyclic peptide with at least one amino acid deleted prior to cyclisation are used to interfere with anglogenesis,

CC cyclisation are used to interfere with anglogenesis,

CC dracacterised by anglogenesis, neovascularisation or lymphanglogenesis.

CC characterised by anglogenesis, neovascularisation or lymphanglogenesis.

CC craum, substance-induced mecvascularisation of the liver, excessive corebrovascular accident, post-regovery

CC craums, substance-induced neovascularisation of the liver, excessive cormone-related anglogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fill decomposed by mammal has a condition characterised by fill decomposed by the accumulation in peripheral limbs or in lumgs, peritoneal cavity, pleurs, cor brain. The peptides are used to image blood vessels and lymphatic vacuulation in peripheral limbs or influenced by VEGF. Cor -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid archite; psoriasis and corrected and and corrected archite; produced archite induced neovascular permeabi
                                                                                                                                                                                                                                                                                                                                                     Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphanglogenesis; psoriasis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 65; DB 4; Length 13;
Pred. No. 0.00033;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 25; Page 47; 102pp; English.
                                                                                                                                                                                                                                                                  Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU04536 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEGF based monocyclic peptide 14.
                                                                                                                                                                                                              (LUDW-) LUDWIG INST CANCER RES
                                                                                              18-JAN-2001; 2001WO-US001533.
                                                                                                                                           18-JAN-2000; 2000US-0176293P.
                                                                                                                                                                    16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CASELGKSTNTFC 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 84.6
Matches 11, Conservative
                                                                                                                                                                                                                                                             Achen MG, Hughes RA,
                                                                                                                                                                                                                                                                                                          WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13 AA;
  WO200152875-A1.
                                               26-JUL-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                               residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU04536;
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Gaps .. 0 ö

gp130; p55;

WO200152875-A1 26-JUL-2001

Achen MG,

residues.

Synthetic

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This sequence is a fragment of feline immunodeficiency virus (FIV) glycoprotein 130. Peptides AAY57038-Y57039 are used in the invention as capture polypeptides when diagnosing FIV infection. The invention relates to an antibody binding composition which consists of an enhanced capture polypeptide, which contains an immunogenic fragment of FIV gag precursor p55, and a second fragment which is part of the env precursor gp130, and an antibody-binding detection composition. The invention also includes a device for performing an assay which determines whether a felline is infected with FIV. The novel method is used for the diagnosis of Feline Immunodeficiency Virus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin binding peptide, autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic;
                                                                                                                                                                                             immunodeficiency virus; FIV; infection; diagnosis; gpl30; p
enic fragment; antibody; env precursor; gag precursor; cat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.4%; Score 32; DB 3; Length 12; 60.0%; Pred. No. 1.38+02; Live 1; Mismatches 3; Indels
                                                                                                                                         Feline immunodeficiency virus env precursor peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diagnosing Feline Immunodeficiency Virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin binding peptide #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O'connor TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABJ04094 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 9; 15pp; English
                                                                                                                                                                                                                                                                                                       Feline immunodeficiency virus.
                                                                                                                                                                                                                                                         antibody binding composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0085615P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99EP-00303760.
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                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||| : | ||
ELGCNONOFC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ELGKSTNTFC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IDEX-) IDEXX LAB INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mermer B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-025671/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200238592-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-1998;
03-JUN-1998;
                                                                                     21-FEB-2000
                                                                                                                                                                                                                                                                                                                                                             EP962774-A1
                                                                                                                                                                                                                            immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Groat RG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ04094;
                                  AAY57039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                             Feline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABJ04094
        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one amonocyclic peptides, dimeric bicyclic peptide with at least one amonocyclic correlation are used to interfere with angiogenesis.

The condition are used to interfere with angiogenesis.

The condition is diabetic retinopathy, psoriamis with a condition of condition is diabetic retinopathy, psoriamis, arthropathy, hemangioma, vascularised malignant or benign tumour, post-recovery correlators are condent, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in aminal (the mammal has a condition characterised by fluid or haring the peptides are also used to modulate vascular permeability or haring the mammal to the mammal to the mammal the mammal to the mamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VEGF, VEGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation, especially rheumatoid arthritis, psoriasis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 4; Length 13;
Pred. No. 0.0016;
3; Mismatches 0; Indels

    13 "This bond cyclises the peptide"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cendron A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 25; Page 47; 102pp; English
                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stacker S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.7%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2000; 2000US-0176293P.
16-MAY-2000; 2000US-0204590P.
                                                                                                                                                                                                                                                                                                                                                       18-JAN-2001; 2001WO-US001533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||::|||||:|
CASDVGKSTNTWC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGKSTNTFC 13
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Best Local Similarity 76.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hughes RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-442248/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13 AA;
                                                                                                                                                             Disulfide-bond
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6

Gaps

; 0

16-MAY-2002.

AAYS7039 standard; peptide; 12 AA.

RESULT 6 AAY57039 ID AAYS'

à g

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The present invention describes a method for diagnosing a disorder characterised by expression of a human cancer associated antigen (CAA) precursor (I) coded by a NA Group I nucleic acid molecule (NI) comprising contacting the biological sample with an agent (A) that specifically binds to NI, (I) or its fragment, complexed with an human leukocyte antigen (HLA) molecule and determining the interaction between the agent and NI or (I). (I) has cytostatic activity and can be used for treating a cherapy and vaccine production. The method can be used for treating a cubject with a condition characterised by expression of (I) in cells of subject with a condition characterised by expression of (I) in cells of subject. AAB75607 and AAB75608 represent proceins from human cancer associated antigen precursors, and AAB75609 to AAB75802 represent HLA class I binding motifs in human cancer associated antigen precursors cycle given in the exemplification of the present invention
        T-cells expressing receptors containing the peptide sequences, which include antigen-specific immunological tolerance to rheumatoid arthritis can be used for the treatment and prevention of rheumatoid arthritis. The invention can be used for the diagnosis, treatment and prevention of rheumatoid arthritis. Sequences AAY6671-958 represent peptides from the various Wheta chains of T cell antigen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing a disorder characterized by expression of a human cancer associated antigen precursor, comprises detecting interaction of an agent with a nucleic acid molecule encoding the antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, cancer associated antigen precursor, cancer associated antigen, seminoma, HLA; human leukocyte antigen; cytostatic; gene therapy;
                                                                                                                                                                                      Gaps
                                                                                                                                                                                      ;
                                                                                                                                                        Length 13;
                                                                                                                                                                                      Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.3%; Score 29; DB 4; Length 10; 60.0%; Pred. No. 3.48+02; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         HLA class I binding motif in HOM-TES-84 SEQ ID NO:29.
                                                                                                                                         DB 3; Leng.
                                                                                                                                                     Score 30; DB 3
Pred. No. 3.1e+
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Page 62; 126pp; English.
                                                                                                                                                                                                                                                                                                                              AAB75626 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfreundschuh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUN-2000; 2000WO-US017207.
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                     5; Conservative
                                                                                                                                                                                                                     17
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                   1 CASELGKSTNTF
                                                                                                                                                                                                                                                CASSIGTNNEOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tureci O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-112465/12.
                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seminoma; HLA; h
vaccine; cancer.
                                                                                                                   Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200100874-A2
                                                                                                                                                                                                                                                                                                                                                                                           10-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                              AAB75626;
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                                                                                                                                                                                                                                                                                               RESULT 9
        8888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor V-beta chain CDR3 region sequences accumulated in anes of rheumatoid arthritis patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to peptide sequences present in the synovial fluid and membranes of rheumatoid arthritis patients, arising from the CDR region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains. Compositions which contain autoantigenic peptides binding specifically to
                                                                                                                                                                       New immunoglobulin-binding peptides, useful for removing autoantibodies
from Serum, e.g. for treating rheumatism, also related solid phases.
                                                                                                                                                                                                                                                   The present invention relates to immunoglobulin binding peptides. These can be used to remove autoantibodies from solutions, particularly autoantibodies associated with autoimmune diseases such as rheumatism, multiple sclerosis and myssthenia gravis, from body fluids. The present sequence is a peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rheumatoid arthritis, arthrosis deformans, T-cell antigen receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 5; Length 13;
Pred. No. 1.4e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wheta chain; autoantigen; immunological tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T cell antigen receptor Vbeta 5 chain peptide.
                                                                                                              Kunze R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 25; 136pp; Japanese.
                                                                                                             Коепареск W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY66781 standard; peptide; 13 AA.
                                                                           (AFFI-) AFFINA IMMUNTECHNIK GMBH.
                                                                                                                                                                                                                     Claim 3; Page 40; 54pp; German.
               08-NOV-2001; 2001WO-EP012933.
                                           08-NOV-2000; 2000EP-00124418,
                                                                                                                                                                                                                                                                                                                                                                                      44.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-JP002814
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                                                                                                                                                                                                                                                                                                                                                                                                                    6, Conservative
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                                                                                                         Winkler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synovial membranes of
                                                                                                                                         WPI; 2002-557447/59.
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N-PSDB; AAZ96511.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CASELGK 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CASHLGK
                                                                                                                                                                                                                                                                                                                                                      Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-APR-2000
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                                                                                                           Egner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY66781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Gaps

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RESULT 10

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Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to immunoglobulin binding peptides. These can be used to remove autoantibodies from solutions, particularly autoantibodies associated with autoimmune diseases such as rheumatism, multiple sclerosis and myasthenia gravis, from body fluids. The present sequence is a peptide of the invention
                                                                                                                                                                                                                                                                                                                                                    New immunoglobulin-binding peptides, useful for removing autoantibodies from serum, e.g. for treating rheumatism, also related solid phases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 5; Length 13;
Pred. No. 4.5e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane dipeptidase-binding lung homing peptide #49.
                                                                                                                                                                                                                                                                                    Kunze R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rajotte D, Pasqualini R, Ruoslahti EI;
                                                                                                                                                                                                                                                                                    Roenspeck W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY48678 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                   (AFFI-) AFFINA IMMUNTECHNIK GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 40; 54pp; German.
                                                                                                                                                                                   08-NOV-2001; 2001WO-EP012933.
                                                                                                                                                                                                                   08-NOV-2000; 2000EP-00124418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US005284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                    Winkler D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prostate, ovary; lymg
membrane dipeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                  WPI; 2002-557447/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CASELGK 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CATHLGK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13 AA;
                                                                                                               WO200238592-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAR-2003
10-DEC-1999
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                                                                                                                                                  16-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY48678;
                                                                                                                                                                                                                                                                                    Egner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
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ID AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to peptide sequences present in the synovial fluid and membranes of rheumatoid arthritis patients, arising from the CDR region of oligoclonal pathogenic T-cell antigen receptor Wbeta chains. Compositions which contain autoantigenic peptides binding specifically to T-cells expressing receptors containing the peptide sequences, which include antigen-specific immunological tolerance to rheumatoid arthritis can be used for the treatment and prevention of rheumatoid arthritis. The invention can be used for the diagnosis, treatment and prevention of rheumatoid arthritis. Sequences AAV66771-958 represent peptides from the various Wbeta chains of T cell antigen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in synovial membranes of rheumatoid arthritis patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                 Rheumatoid arthritis, arthrosis deformans, T-cell antigen receptor; Vbeta chain; autoantigen; immunological tolerance.
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Pred. No. 4.5e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                 T cell antigen receptor Wheta 10 chain peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 29; 136pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä.
                                                                                                                                AAY66787 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-JP002814.
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98JP-00328761.
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                 13
                                     CASSKGTST 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-086978/07.
               ELGKSTNTFC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      WO9963084-A1.
                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-1998;
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Matches
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RESULT 11

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13-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                              AAE26783
8
                                                                                                                            The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue is identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adreanal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP) AAY48618 to AAX49066 represent sequences which are used in the exemplification of the present invention. (Updated on 20-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel tumor-associated antigen, designated 9D7 which has cycostatic activity. The invention also describes a method for isolating (al a polypeptide (I) that includes (81) as part of its sequence; (b) an immunogenic protein fragment or peptide (II) derived from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7, (l) as active ingredients; (d) an isolated DNA (III) encoding a protein (IV) with the immunogenic properties of 9D7 or its fragments; (e) a recombinant DNA (IIIa) that includes (III); and (f) antibodies (Ab) directed against 9D7, (1) or (II). 9D7, or its derived immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for immunotherapy of cancer
                                        New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;
lung; colon; breast; carcinoma; Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                     Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tumor-associated antigen 9D7, useful e.g. for immunand for producing diagnostic or therapeutic antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human 9D7 protein immunogenic fragment SEQ ID NO: 55.
                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 2; I
Pred. No. 1.4e+06;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                                                              Example 6; Page 144; 193pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB10896 standard; protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 45; 50pp; German.
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71.4%;
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         WPI; 1999-571717/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                    7 KSTNTFC 13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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peptides, are used to induce a humoral and/or cellular response for use in in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7 can be used similarly and cells that express 9D7 are useful in cellular anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for imaging, diagnosing and monitoring cancers, also, when conjugated to cytotoxins or radiomuclide, as therapeutic agents. Peptides derived from 9D7 may also be used diagnostically to test for an immune response. 9D7-associated cancers are particularly kidney, lung, colon and breast carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic fragments of the human tumor-associated antigen 9D7 which is described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis; myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic; ansemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder; inflammatory disorder; anglogenesis; stroke; cerebroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a synthetic fibrin binding group having affinity for fibrin. The invention is useful for detecting fibrin in a mammalian subject which involves (a) detectably labelling the binding group; (b) administering to the subject the labelled polypeptide, and (c) detecting the labelled polypeptide in the subject. The invention is useful for treating a disease involving thrombus formation eg. deep-vent thrombosis, pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial for detection, imaging and localisation of fibrin-containing clots by magnetic resonance imaging, radioimaging and other imaging methods and are also useful in the diagnosis and treatment of coronary conditions where fibrin plays a role. The fibrin binding moieties are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel synthetic fibrin-binding moiety, useful for detecting, imaging or localizing fibrin-containing clots by magnetic resonance imaging, radioimaging and for treating diseases involving thrombus formation e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE26783 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.9%;
71.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fibrin binding peptide #36.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 AA;
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detecting and diagnosing numerous pathophysiologies in which fibrin plays a role eg. peritoneal adhesions which often occur after surgery or inflammatory and neoplastic processes and are comprised of a fibrin network, fibroblasts, macrophages and new blood vessels; rheumatoid
                                                                                                                arthritis, lupus or septic arthritis which often have bits of fibrin containing tissues called rice bodies in the synovial fluid of their joints; thrombocytopenic purpura, a type of anaemia in which deposits in arterioles causes turbulent blood flow resulting in stress and destruction of red blood cells. The fibrin specific agents can also be used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain retinopathy, early or high-risk atherosclerosis and other autoimmune and inflammatory disorders. Fibrin specific agents also could provide both direct or surrogate markers of disease models in which hypoxia and anglogenesis are expected to play a role. The invention is also useful for screening molecular libraries. The present sequence is a fibrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
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Score 28; DB 5; Length 9; Pred. No. 1.4e+06; 2; Mismatches 2; Indels 38.9%; 50.0%; 4; Conservative 6 GKSTNTFC 13 |: : ||| 2 GOESRIFC 9 Query Match Best Local Similarity Matches 4; Conserv à

AAB10895 standard; protein; 10 AA. (first entry) 26-JAN-2001 AAB10895;

Tumor-associated antigen, 9D7; human; cytostatic; immunogenic; immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney; lung; colon; breast; carcinoma; Hodgkin's lymphoma. Human 9D7 protein immunogenic fragment SEQ ID NO: 54.

DE19909503-A1. Homo sapiens.

99DE-01009503. 04-MAR-1999; 07-SEP-2000.

(BOEH) BOEHRINGER INGELHEIM INT GMBH.

99DE-01009503

04-MAR-1999;

Klade C, Adolf G, Sommergruber W, Heider K;

WPI; 2000-588357/56.

This invention describes a novel tumor-associated antigen, designated 9D7 which has cytostatic activity. The invention also describes a method for isolating (a) a polypeptide (I) that includes (S1) as part of its sequence; (b) an immunogenic protein fragment or peptide (II) derived from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7, (I) or (II) as active ingredients; (d) an isolated DMA (III) encoding a protein (IV) with the immunogenic properties of 9D7 or its fragments; (e) a recombinant DNA (IIIa) that includes (III); and (f) antibodies (Ab) directed against 9D7, (I) or (II). 9D7, or its derived immunogenic New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer and for producing diagnostic or therapeutic antibodies. Claim 6; Page 45; 50pp; German.

peptides, are used to induce a humoral and/or cellular response for use in in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 907 can be used similarly and cells that express 907 are useful in cellular anticancer vaccines. Antibodies (Ab) specific for 907 are useful for imaging, disagnoshing and monitoring cancers, also, when conjugated to cytocoxins or radiomucilde, as therapeutic agents. Peptides derived from 907 may also be used diagnostically to test for an immune response. 907-associated cancers are particularly kidney, lung, colon and breast carcinoma and Hodgkin's lymphoma. ABB10899 represent immunogenic fragments of the human tumor-associated antigen 907 which is described in the method of the invention 883888888888888

Sequence 10 AA;

Gaps .; 0 Score 28; DB 3; Length 10; Pred. No. 5.1e+02; 0; Mismatches 2; Indels 38.9%; 71.4%; 5; Conservative Query Match Best Local Similarity Matches

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4 CGSRLGK 10 1 CASELGK 7 ઠ

Search completed: March 8, 2004, 11:54:09 Job time : 55 secs

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Gaps ô

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1: /cgm2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgm2_6/ptodata/2/pubpaa/PCT7_NBW PUB.pep:*

3: /cgm2_6/ptodata/2/pubpaa/PCT NBW PUB.pep:*

4: /cgm2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgm2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

6: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

7: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 5, Appli	Sequence 15, Appl	Sequence 16, Appl	Sequence 18, Appl	Sequence 17, Appl	Sequence 14, Appl	Sequence 55. Appl	Sequence 626, App	Sequence 19, Appl	Sequence 262, App	Sequence 262, App	Sequence 67. Appl	Seguence 67, Appl	Sequence 140, App	Sequence 572, App
SUMMARIES	QI	US-09-761-636A-5	US-09-761-636A-15	US-09-761-636A-16	US-09-761-636A-18	US-09-761-636A-17	US-10-208-304-14	US-10-034-974-55	US-09-573-822C-626	US-10-271-343-19	US-09-791-393-262	US-09-791-389-262	US-10-322-210-67	US-10-304-443-67	US-09-795-006A-140	US-10-117-937-572
	DB	6	σ	9	σ	σ	14	14	10	14	10	10	14	14	σ	15
	Query Match Length DB	13	13	13	13	13	10	თ	10	10	12	12	13	13	80	6
æ	Query Match	100.0	95.8	90.3	90.3	84.7	41.7	38.9	37.5	37.5	37.5	37.5	37.5	37.5	36.1	36.1
	Score	72	69	65	9	61	30	28	27	27	27	27	27	27	26	56
	Result No.	1	7	m	ব	2	9	7	80	σ	10	11	12	13	14	15

; 0

> ; Sequence 15, Application US/09761636A ; Patent No. US20020065218A1

RESULT 2 US-09-761-636A-15

Sequence 70, Appl			956,		13,	Sequence 15, Appl	16,	573	26,	17,		35,	57,	32,	150,	190,	5800,	5983,	6053,	6355,	Sequence 6654, Ap	Sequence 6792, Ap	706	77, A	122	5,	Sequence 2991, Ap	96	
US-10-044-844-70	US-09-572-404B-2743	US-09-572-404B-3191	US-09-572-270A-956	US-10-208-304-12	US-10-208-304-13	US-10-208-304-15	US-10-208-304-16	US-10-117-937-573	US-09-792-686A-26	US-10-271-343-17	US-09-792-686A-28	US-10-148-786A-35	US-10-046-922-57		US-10-281-478-150	US-10-114-669-190	US-10-114-669-5800	US-10-114-669-5983	US-10-114-669-6053	US-10-114-669-6355		US-10-114-669-6792	US-10-114-669-7062	US-10-449-659-77	US-10-324-143-122	US-09-747-802-5	US-09-880-748-2991	US-10-239-313A-96	US-10-348-232-224
15	10	10	10	14	14	14	14	15	10	14	10	14	13	14	14	15	15	15	15	15	12	15	15	15	15	10	10	14	14
9	10	10	10	10	10	10	10	10	13	10	13	13	10	80	œ	10	10	10	10	10	10	10	10	11	11	13	13	∞	6 0
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26	26	26	26	26	26	26	26	26	26	25	25	25	24.5	24	24	24	24	24	24	24	24	24	24	24	24	24	24	23	23
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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US-09-761-636A-5;

SQUENCE S. Application US/09761636A;
Patent No. US2002065218A1
GENERAL INFORMATION:
Patent No. US2002065218A1
GENERAL INFORMATION:
PAPPLICANT: ACHEN, Marc
APPLICANT: ACHEN, Mace
APPLICANT: CENDRON, Angela
TITLE OF INVENTION, Angela
TITLE OF INVENTION UNMERR: US/09/761,636A
CURRENT APPLICATION NUMBER: US 60/176,293
FRIOR APPLICATION NUMBER: US 60/176,293
FRIOR APPLICATION NUMBER: US 60/176,293
FRIOR APPLICATION NUMBER: US 60/204,590
PRIOR PLING DATE: 2000-01-18
PRIOR PLING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
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SOFTWARE: ACHE SAMINATION OF SECONS OF THE SAMINATION OF SECONS OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09761636A;
Sequence 17, Application US/09761636A;
Batent No. US2020065218A1
GENERAL INFORMATION:
APPLICANT: STACKER, Marc
APPLICANT: HUGHES, Richard
APPLICANT: CHORNON, Angela
TITLE OF INVENTION: VBGF-D/VBGF-C/VBGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A;
CURRENT APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-01-18
PRIOR PRILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFFWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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TITLE OF INVENTION: VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR FILE REPERENCE: 1064/48505 Achen et al CURRENT APPLICATION NUMBER: 026/99/761,636A CURRENT FILING DATE: 2001-01-18 PRIOR PELICATION NUMBER: US 60/176,293 PRIOR FILING DATE: 2000-01-18 PRIOR FILING DATE: 2000-01-18 PRIOR PILING DATE: 2000-01-16 NUMBER: 05 SEQ ID NOS: 34 SOFTWARE: PATCHTING DATE: 2000-05-16 NUMBER: PATCHTING DATE: 2000-05-16 SOFTWARE: PATCHTING DATE: 2000-05-16 NUMBER: PATCHTING DATE: PATCHTING DATCHTING DATE: PATCHTING DATE: PATCHTING DATCHTING DATE: PATCHTING DATE: PATCHTING DATCHTING DATE: PATCHTING DATCHTING DATCHTING D
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Pred. No. 6.9e-05;
2; Mismatches 0; Indele
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APPLICANT: Lechleider, Robert J.
APPLICANT: Stobris, Anita B.
APPLICANT: Yi, Youngauk
TITLE OF INVENTION: NOVEL HUMAN SEPTIN AND USES THEREFOR
FILE REFERENCE: 11613.42USH.
CURRENT FILING DAIE: 2002-07-29
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Publication No. US20030124571A1
SERREAL INFORMATION:
APPLICANT: Larisch, Sarit
APPLICANT: Kim, Seong-Jin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.7%;
76.9%;
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; ORGANISM: synthetic construct
US-09-761-636A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: synthetic construct US-09-761-636A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.3%;
Best Local Similarity 84.6%;
Matches 11; Conservative
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Best Local Similarity 76.9
Matches 10; Conservative
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US-09-761-636A-17
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US-10-208-304-14
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US-09-561-636A-16
Sequence 16, Application US/09761636A
Sequence 16, Application US/09761636A
Patent No. US20020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, Marc
APPLICANT: HUGHES, Richard
PAPLICANT: HUGHES, Richard
PAPLICANT: CENDRON, Angele
TITLE OF INVENTION: VAGE-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR APPLICATION NUMBER: US 60/176,293
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
SEQ ID NO 16
SEQ ID NO 16
LENGTH: 13
                                                APPLICANT: ACHEN, Marc
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: STACKER, Steven
APPLICANT: GENERAL
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGF-D/VEGF-PEPTIDOMIMETIC INHIBITOR
FILE REFERENCE: 1064/48505 Achen et al
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2001-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3:0
SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69; DB 9; Length 13;
Pred. No. 1.4e-05;
1; Mismatches 0; Indels
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US-09-761-636A-18
SQUE-09-761-636A-18
SQUE TO USZ0020065218A1
GENERAL INFORMATION:
APPLICANT: ACHEN, MATC
APPLICANT: STACKER, Steven
APPLICANT: HUGHES, Richard
APPLICANT: CENDRON, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: synthetic construct
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Best Local Similarity 92.3%;
Matches 12; Conservative
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US-09-761-636A-15
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APPLICANT: Skelton, Nicholas J.
APPLICANT: Skelton, Nicholas J.
APPLICANT: Skelton, Nicholas J.
APPLICANT: Starovasnik, Melissa A.
TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES;
TITLE OF INVENTION: ON PHAGE;
CURRENT APPLICATION NUMBER: US(10/271,343)
CURRENT PLING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 69/592,695
PRIOR RILNG DATE: 2000-06-13
PRIOR APPLICATION NUMBER: US 60/139,017
PRIOR APPLICATION NUMBER: US 60/139,017
PRIOR PRINTED DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 60
SEQ ID NOS: 60
LENGTH: 10
                        ; OTHER INFORMATION: Sequence located in MG309 at 847-856 and may interact with Sequity OTHER INFORMATION: in this patent.
US-09-573-822C-626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 262, Application US/09791393
| Publication No. US20030032200A1
| GENERAL INFORMATION:
| APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
| APPLICANT: Pareth, Rajesh Bhikhu
| APPLICANT: Rohlff, Christian
| TITLE OF INVENTION: Proteins, Genes and Their Use for TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
| TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
| TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
| TITLE OF INVENTION: DATE: US/09/791,393
| CURRENT FILING DATE: 2002-01-02
| EARLIER APPLICATION NUMBER: GB 0004412.3
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                                                                                                                             Length 10;
                                                                                                                                                                                1; Indels
                                                                                                                          37.5%; Score 27; DB 10;
40.0%; Pred. No. 2.8e+02;
tive 5; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                US-10-271-343-19; Septication US/10271343; Sequence 19, Application US/10271343; Publication No. US20030166003A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (5)...(5)
OTHER INFORMATION: Xaa is D-pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE: OTHER INFORMATION: Turn Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                             Query Match
Best Local Similarity 40.0%
....hes 4; Conservative
                                                                                                                                                                                                                                                                1 AKLSRTINSF 10
                                                                                                                                                                                                                                  3 SELGKSTNTF 12
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                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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Sequence 626, Application US/09573822C

Sequence 626, Application US/09573822C

Sequence 626, Application No. 920030199011A1

GENERAL INFORMATION:
APPLICANT: Proteom Ltd

TITLE NOF INVENTION: Complementary peptide ligands generated from microbial genome seq
FILE REFERENCE: Microbe patent
CURRENT APPLICATION NUMBER: US/09/573,822C

NUMBER OF SEQ ID NOS: 804

SOFTWARE: PACPALENT version 1.0

SEQ ID NO 626

LENGTH: 10

TYPE: PRT

CRANISM: mycoplasma genitalium
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US-10-034-974-55
| Sequence 55, Application US/10034974
| Publication No. US20030143158A1
| Publication No. US20030143158A1
| GENERAL INCORMATION:
| APPLICANT: DYAX CORP.
| APPLICANT: Beltzer, James P.
| APPLICANT: Bescott, Charles R.
| APPLICANT: Bescott, Charles R.
| APPLICANT: Bescott, Charles R.
| TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
| FILE REFERENCE: DYX-024.1 PCT; DXX-024.1 US
| CURRENT FILING DATE: 2001-12-21
| PRIOR APPLICATION NUMBER: US 09/747,403
| NUMBER OF SEQ ID NOS: 56
| SOFTWARE: Patentin version 3.1
| IRNOTH- OS
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Pred. No. 83;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: , OTHER INFORMATION: fibrin binding polypeptides US-10-034-974-55
PRIOR APPLICATION NUMBER: PCT/USO1/02466
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 60/178,866
PRIOR FILING DATE: 2000-01-29
PRIOR FILING DATE: 2000-01-29
PRIOR PLING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                41.7%;
87.5%;
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Best Local Similarity 87.5
Matches 7; Conservative
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US-10-208-304-14
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HITLE OF INVENTION: Thereof, and Their Therapeutic Uses
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smithkline Beecham Biologicals s.a.
APPLICANT: Peptide Therapeutics Ltd.
TITLE OF INVENTION: Vaccine
CURRENT APPLICATION NUMBER: US/10/304,443
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US/09/698,906A
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 121
SEQ ID NOS: 121
SEQ ID NO 67
SEQ ID NO 67
                  FILE NETREBREE: 845173

CURRENT FILING DATE: 2002-12-18

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: US/10/322,210

CURRENT PILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: GB 9904406.3

PRIOR FILING DATE: 1999-02-25

PRIOR FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: GB 9917144.9

PRIOR FILING DATE: 1999-08-07

PRIOR PLING DATE: 1999-08-07

PRIOR PRIOR PLING DATE: 1999-08-07

PRIOR PRIOR PLING DATE: 1999-08-07

PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR
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ORGANISM: Human peptide sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTHER INFORMATION: Chimeric US-10-322-210-67
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Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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US-09-795-006A-140
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S. 29-79-12-89-262

j. Sequence 262, Application US/09791389

j. Bublication No. US2003003277341

j. Sequence 1262

j. Sequence 262, Application US/09791389

j. Publication No. US2003003277341

j. APPLICANT: Horakarino:
    APPLICANT: Parekh, Reistian Mikhu

APPLICANT: Parekh, Rajesh Bhikhu

APPLICANT: Terret, Jonathan Alexander

TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)

TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder

TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder

TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder

TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder

TITLE OF INVENTION NUMBER: US/09/791,389

CURRENT APPLICATION NUMBER: GB 0030050.9

PRIOR FILING DATE: 2000-12-08

PRIOR FILING DATE: 2000-12-08

PRIOR FILING DATE: 2000-12-08

PRIOR FILING DATE: 2000-12-08

SOFTWARE: ReatSEQ for Windows Version 4.0

SEQ ID NO 262

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Publication No. US20030147906A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Turnell, William Gordon
APPLICANT: Turnell, William Gordon
APPLICANT: Van Mechelen, Marcelle Paulette
APPLICANT: Vinals y de Bassole, Carlore
TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IgB, Antagonists
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HARLIER FILING DATE: 2000-02-24
FRALIER PEPLICATION NUMBER: GB 0030050.9
EARLIER FILING DATE: 2000-12-08
EARLIER FILING DATE: 2000-12-08
HARLIER FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 308
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 262
LENGTH: 12
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US-09-791-393-262
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US-09-791-389-262
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CTTELGR 12
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Matches 4; Conserv
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US-10-322-210-67
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Sequence 140, Application US/09795006A

Patent No. US20020151680A1

GENERAL INFORMATION:

APPLICANT: Alitalo et al

TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS

TITLE OF INVENTION: BNDCHHELIAL GROWTH FACTOR DNAS AND PROTEINS

FILE REFERENCE: 289671359778

CURRENT FILING DATE: 2001-02-26

PRIOR FILING DATE: 2000-05-18

PRIOR PLICATION NUMBER: US 60/185,205

PRIOR PLICATION NUMBER: US 60/185,205

PRIOR FILING DATE: 2000-05-18

SEQ ID NOS: 175

SEQ ID NO 140

LENGTH: 8

MATERIAL OF THE OFFICE 
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Best Local Similarity 66.7%; Pred. No. 7.2e+05;
Matches 4; Conservative 1; Mismatches 1; Indels
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Sequence 572, Application US/10117937
Publication No. US2003022039A1
GENERAL INFORMATION:
APPLICANT: TEL IMMOND THERAPIES CORP.
APPLICANT: DIAMOND, David, C.
APPLICANT: LIU, Liping
APPLICANT: LIU, Liping
APPLICANT: APPLICANT: ALIO, APPLICANT: APPLI
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Job time : 32 secB
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CORGANISM: Homo sapiens
US-10-117-937-572
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| EFGVATNT 8
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US-10-117-937-572
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55, Appl
66, Appl
58, Appl
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12, Appl
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                                                                                                                               March 8, 2004, 11:45:28 ; Search time 23 Seconds
   (without alignments)
   51.626 Million cell updates/sec
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1. /cgn2_6/pcdata/2/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4. /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

5. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*

6. /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-742-243-64

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US-08-742-243-65

US-08-742-243-65

US-08-742-243-59

US-08-742-243-59

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US-08-742-243-59

US-08-742-243-59

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US-08-972-922B-12

US-08-972-922B-26

US-08-972-922B-26

US-08-972-928-26

US-08-97-992B-26

US-08-97-992B-26

US-08-97-992B-26

US-08-97-992B-26

US-08-97-992B-26

US-08-97-992B-15

US-08-97-992B-15

US-08-97-992B-15

US-08-97-992B-15

US-08-97-992B-13

US-08-97-992B-13

US-08-97-992B-13

US-08-97-992B-13

US-08-97-97-978-143

US-08-484-631-143

US-08-484-631-143

US-08-484-631-143

US-08-97-570-143
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                                                                                                                                                                                                                                            133
1 QGQHIGEMSFLQHNKCECRPKKD 23
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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seq length: 23
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Maximum DB 6
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Sequence 31, Appl	Sequence 32, Appl	Sequence 33, Appl	Sequence 34, Appl	Sequence 35, Appl	Sequence 36, Appl	Sequence 37, Appl	Sequence 38, Appl	Sequence 5, Appli	-	Sequence 25, Appl	Sequence 25, Appl	Sequence 25, Appl		Sequence 81, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 11, Appl	
15 2 US-08-752-852A-31	15 2 US-08-752-852A-32	15 2 US-08-752-852A-33	15 2 US-08-752-852A-34	. 7	15 2 US-08-752-852A-36	15 2 US-08-752-852A-37	15 2 US-08-752-852A-38	20 3 US-08-786-690-5	4	22 3 US-08-782-480-25	22 3 US-08-954-211-25	4	22 4 US-09-176-741B-25	12 2 US-08-244-496-81	13 4 US-09-479-479-12	13 4 US-09-297-851-12	14 3 US-08-991-426-11	ALIGNMENTS
28 33 24.8	29 33 24.8	33	33	32 33 24.8	33	34 33 24.8	35 33 24.8		37 32 24.1	32	39 32 24.1	32	41 32 24.1	42 31 23.3	31	31	31	

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Sequence 25, Application US/08807992B
Patent No. 602541
GENERAL INFORMATION:
APPLICANT: Senger, Donald R
APPLICANT: Senger, Donald R
APPLICANT: Senger, Donald R
TITLE OF INVENTION: percellic binding to spatially exposed regions of vascular TITLE OF INVENTION: percellic binding to spatially exposed regions of vascular TITLE OF INVENTION: percellity factor bound in-vivo to a tumor associated blook TITLE OF INVENTION: vessel
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: David Prashker, Esq.
STREET: P.O. Box 5387
CITY: Magnolia
STREET: P.O. Box 5387
CITY: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.7%; Score 82; DB 3; Length 17;
100.0%; Pred. No. 3.1e-06;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette, 3.50 inch, 1.40 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/1
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,992B
FILING DATE: March 3, 1997
CLASSIFICATION: 424
ATTORNEY, AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,6933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: BIS-033
TELECOMONICATION INFORMATION:
TELEPHONE: (978) 525-3794
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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MEDIUM TYPE: Diskett
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RESULT 1
US-08-807-992B-25
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Best Local Similarity 100. Matches 15; Conservative

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Gaps ; 0

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3 QGQHIGEMSFLQHNK 17

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: synthesized ; OTHER INFORMATION: peptide fragment US-08-742-243-2
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Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Matesumoto, Tomoe
APPLICANT: Okamoto, Masaji
APPLICANT: Okamoto, Masaji
APPLICANT: Suzuki, Hidoe
TITILE OF INVENTION: Peptides And Monoclonal Antibodies
FILE REFERENCE: 07898/005001
CURRENT PILING DATE: 1996-10-31
CURRENT FILING DATE: 1995-11-01
NUMBER OF SEQ ID NOS: 70
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 63
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12,
                                                                | PACENT NO. 0024393
| PACENT NO. 0024393
| APPLICANT: ABANCO
| APPLICANT: Yukita, Ayakoto
| APPLICANT: Witia, Ayakoto
| APPLICANT: Watasumoto, Tomoe
| APPLICANT: Watasumoto, Tomoe
| APPLICANT: Okamoto, Massji
| APPLICANT: Okamoto, Massji
| APPLICANT: OR 1991 (1990)
| TITLE OF INVENTION: PEPTIGES And MONOCLONAL ANTIONAL OF INVENTION NUMBER: US/08/742,243A
| CURRENT APPLICATION NUMBER: 308184/1995
| BARLIER FILING DATE: 1996-10-31
| NUMBER OF SEQ ID NOS: 70
| SEQ ID NOS: 70
| SEQ ID NO SEQ ID NOS: 70
| SEQ ID NO SEQ ID NOS: 70
| SEQ ID NO SEQ ID NOS: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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54.9%; Score 73; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 5.4e-05;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-742-243-63
Sequence 63, Application US/08742243A
Parent No. 6024955
GENERAL INFORMATION: ARCLO
APPLICANT: ABRADO, MAKCLO
APPLICANT: Yukita, Ayako
APPLICANT: Hanatani, Miteuya
US-08-742-243-2
; Sequence 2, Application US/08742243A
; Patent No. 6024955
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1 Similarity 100.0%; Pred. No. 5.4e-05;
12; Conservative 0; Mismatches 0; Indels
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APPLICANT: Mancho, Makoto
APPLICANT: Mancho, Miteuya
APPLICANT: Hanchani, Miteuya
APPLICANT: Mareaunico, Tomoe
APPLICANT: Mareaunico, Tomoe
APPLICANT: Offensor, Masaji
APPLICANT: Okamoto, Masaji
APPLICANT: Okamo
                                                                                                                                                                                                                                                                                                               GENERAL INFORTATION,
MAKOLO
APPLICANT: AGAIO, MAKOLO
APPLICANT: ANALIA, Ayako
APPLICANT: Matasumoto, Tomoe
APPLICANT: Matasumoto, Tomoe
APPLICANT: Suzuki, Hideo
APPLICANT: Ournet, Masaji
APLICANT: Suzuki, Hideo
TITLE OF INVENTION: Peptides And Monoclonal Antibodies
FILE REPERENCE: 07989/005001
CURRENT APPLICATION NUMBER: US/08/742,243A
CURRENT APPLICATION NUMBER: 1996-10-31
EARLIER APPLICATION NUMBER: 308184/1995
EARLIER FILING DATE: 1995-11-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
LENGTH: ABANCH: ABA
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; Sequence 62, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
RESULT 4
US-08-742-243-64
US-08-742-243-64
; Sequence 64, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 12; Conserva
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FRATURE: OTHER INFORMATION: Description of Artificial Sequence: synthesized OTHER INFORMATION: peptide fragment
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                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Asano, Maketo
APPLICANT: Asano, Maketo
APPLICANT: Yukita, Ayako
APPLICANT: Hanatani, Mitsuya
APPLICANT: Matasumoto, Tomoe
APPLICANT: Matasumoto, Tomoe
APPLICANT: Okamoto, Masaji
APPLICANT: Suzuki, Hideo
ITILE OF INVENTION: Peptides And Monoclonal Antibodies
FILE REPERENCE: 07898/00501
CURRENT APPLICATION NUMBER: US/08/742,243A
CURRENT FILING DATE: 1996-10-31
EARLIER PILING DATE: 1995-11-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 12
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GENERAL INFORMATION:
APPLICANT: ABANC, Makoto
APPLICANT: Tukita, Ayako
APPLICANT: Hanatani, Mitsuya
APPLICANT: Hanatani, Mitsuya
APPLICANT: Hanatanioto, Tomoe
APPLICANT: Okamoto, Masaji
APPLICANT: Suzuki, Hideo
TITLE OF INVENTION: Peptideo
TITLE REFERENCE: 07898/005001
CURRENT FILING DATE: 1996-10-31
FEALIER APPLICATION NUMBER: 30818/1995
FALIER APPLICATION NUMBER: 30818/1995
FALIER APPLICATION NUMBER: 30818/1995
SALIER PRILOGATION NUMBER: 30818/1995
SALIER PRILOGATION NUMBER: 30818/1995
SELING DATE: 1995-11-01
SOFTWARE: PATENTION OF: 2.0
SOFTWARE: PATENTION OF: 2.0
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                           5 IGEMSFLOHNKC 16
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Best Local Similarity
                                                                                                                                                                                                         RESULT 8
US-08-742-243-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: synthesized OTHER INFORMATION: peptide fragment
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GENERAL INFORMATION:

APPLICANT: ASANO, Maketo
APPLICANT: Yukita, Ayako
APPLICANT: Yukita, Ayako
APPLICANT: Hanatani, Mitsuya
APPLICANT: Hanatani, Mitsuya
APPLICANT: Okamoto, Masaji
APPLICANT: Okamoto, Masaji
APPLICANT: Okuki, Hideo
ITILE OF INVENTION: Peptideo
ITILE OF INVENTION: Peptideo
ITILE APPLICATION NUMBER: US/08/742,243A
CURRENT APPLICATION NUMBER: US/08/742,243A
CURRENT FILING DATE: 1996-10-11
KRALIER APPLICATION NUMBER: 1995-11-01
KRALIER PILING DATE: 1995-11-01
KNUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6: ILENDER PRODUCT OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Matasumoto, Tome
APPLICANT: Okamoto, Masaji
APPLICANT: Okamoto, Masaji
APPLICANT: Okamoto, Masaji
TITLE OP INVENTION: Peptides And Monoclonal Antibodies
FILE REFERENCE: 07898/005001
CURRENT APPLICATION NUMBER: US/08/742,243A
CURRENT APPLICATION NUMBER: 308184/1995
BARLIER APPLICATION NUMBER: 308184/1995
BARLIER FILING DATE: 1995-11-01
NUMBER OF SEQ ID NOS: 70
SOFWARE: Patentin Ver: 2.0
                                                                                                                                                                          RESULT 6
US-08-742-243-65
Sequence 65, Application US/08742243A
Patent No. 6024955
GENERAL INFORMATION:
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Patent No. 6024955
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Asano, Makoto
APPLICANT: Yukita, Ayako
APPLICANT: Hanatani, Mitsuya
7 EMSFLOHNKCEC 18
                                                                  1 EMSFLQHNKCEC 12
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Sequence 9, Application US/08807992B

Sequence 9, Application US/08807992B

Patent No. 6022541

GORDERAL INFORMATION:
APPLICANT: Senger, Donald R

APPLICANT: Dvorak, Harold F

TITLE OF INVENTION: Immunological preparation for concurrent

TITLE OF INVENTION: Specific binding to spatially exposed regions of vascular

TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated bloom

TITLE OF INVENTION: 11

NUMBER OF SEQUENCES:
ADDRESSE: David Prashker, Esq.
STREET: P.O. Box 5387

CITY: Magnolia
STREET: B.O. Box 5387

CITY: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description of Artificial Sequence: synthesized CTHER INFORMATION: peptide fragment US-08-742-243-58
                                                                                                                                                                                                                                                                   US-08-742-243-58

US-08-742-243-58

Sequence 58, Application US/08742243A

Patent No. 602455

GENERAL INFORMATION:

APPLICANT: Hanatani, Makoto

APPLICANT: Hanatani, Mitsuya

APPLICANT: Hanatani, Mitsuya

APPLICANT: Matamundto, Tomoe

APPLICANT: Suzuki, Hideo

APPLICANT: Suzuki, Hideo

TITLE REFERENCE: 07898/005001

CURRENT APPLICATION NUMBER: US/08/742,243A

FILE REFERENCE: 07898/005001

CURRENT FILING DATE: 1995-11-01

MUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 58

LENGTH: 12

LENGTH: 12
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40.6%; Score 54; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage COMPUTER: IBM P8/1
COMPUTER: IBM P8/1
OPERATING SYSTEM: MS DOS SOFTWARE: WORDERFECT VERSION 5.1
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/807,992B
FILING DATE: March 3, 1997
CLASSIFICATION: 424
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Description of Artificial Sequence: synthesized
CHERR INFORMATION: peptide fragment
US-08-742-243-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
O'THER INFORMATION: Description of Artificial Sequence: synthesized
O'THER INFORMATION: peptide fragment
US-08-742-243-3
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Sequence 66, Application US/08742243A

Patent No. 6024955

GENERAL INFORMATION:
APPLICANT: Asano, Makoto
APPLICANT: Vakita, Ayako
APPLICANT: Watasumoto, Tomoe
APPLICANT: Matasumoto, Tomoe
APPLICANT: Matasumoto, Tomoe
APPLICANT: Matasumoto, Massji
APPLICANT: Okamoto, Massji
APPLICANT: Okamoto, Massji
APPLICANT: Okamoto, Massji
APPLICANT: Oraxki, Hideo
ITILE OF INVENTION: Peptides And Monoclonal Antibodies
FILE REPERENCE: 079394/05001
CURRENT FILING DATE: 1996-10-31
BARLIER APPLICATION NUMBER: 308184/1995
BARLIER PILING DATE: 1995-11-01
NUMBER OF SEQ ID NOS: 70

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 66

IRMOTATION OF
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42.1%; Score 56; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Vaxita, Agako
APPLICANT: Yukita, Ayako
APPLICANT: Hanatani, Mitsuya
APPLICANT: Hanatani, Mitsuya
APPLICANT: Hanatani, Mitsuya
APPLICANT: Matasumoto, Tomoe
APPLICANT: Okamoto, Masaji
APPLICANT: Suzuki, Hideo
TITLE OF INVENTION: Peptides And Monoclonal Antibodies
FILE REPERRENCE: 07898/00501
CURRENT APPLICATION NUMBER: US/08/742,243A
CURRENT FILING DATE: 1996-10-31
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3: SEQ ID NO 3
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                         Mismatches
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; Sequence 3, Application US/08742243A
; Patent No. 6024955
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                            12; Conservative
                                                                                                                                     1 OGOHIGEMSFL0 12
                                                                                             1 OCCHIGEMSFLO 12
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                            Matches
                                                                                                                                                                                                                                                                       RESULT 10
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Query Match

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Gaps

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38.3%; Score 51; DB 1; Length 18; 100.0%; Pred. No. 0.2;
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                             RESULT 15
US-08-327-709-2
US-08-327-709-2
SEQUENCE 2, Application US/08327709
Patent No. 5659013
GENERAL INFORMATION:
APPLICANT: Donald R. Senger and Harold F.
APPLICANT: TAKETED COMPOUNDS
NUMBER OF SEQUENCES: A SCHEET CORRESPONDENCE ADDRESSE: Fish & Richardson STREE: Assachusetts
CORRESP. 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTER FRADABLE FORM:
ALL ZIE: 02110-2804
COMPUTER FRADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/327,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Job time : 24 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/779,384
FILING DATE: OCTOBER 18, 1991
ATTORNEX/AGENT INFORMATION:
NAME: CLARK, PAUL T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 01948/02
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
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Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
TELEX: 20
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APPLICANT: Senger, Donald R
APPLICANT: Senger, Donald R
APPLICANT: Senger, Donald R
APPLICANT: Senger, Donald F
TITLE OF INVENTION: Immunological preparation for concurrent
TITLE OF INVENTION: permeability factor bound in-vivo to a tumor associated blood
TITLE OF INVENTION: vessel
NUMBER OF SEQUENCES: 31
CORRESPONDENCS:
ADDRESSEE: David Prashker, Esq.
STRRET: P.O. Box 5387
CITY: Magnolia
STRATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.3%; Score 51; DB 3; Length 14; Best Local Similarity 100.0%; Pred. No. 0.15; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: OCHOUTER READABLE FORM:
MEDIUM TYPER Dibkette, 3.50 inch, 1.40 Mb storage COMPUTER: IRM PS/1
COMPUTER: IRM PS/1
COMPUTER: IRM PS/1
COMPUTER: IRM PS/1
COMPUTER: IRM PS/1
COMPUTER: IRM PS/1
CURRENT APPLICATION DAPA:
TILING DAPE: March 3, 1997
CLASSIFICATION 1424
ATTORNEY/AGENT INFORMATION:
NAME: DAYL BREAKEY, ESG.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: 29,693
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICA
ATTORNEY/AGENT INFORMATION:
NAME: David Prashker, Esq.
REGISTRATION NUMBER: 29,693
REFERENCE/DOCKET NUMBER: BIS-033
TELECOMMUNICATION INFORMATION:
TELECHOME: (9798) 525-3794
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08807992B Patent No. 6022541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 8, Conservative
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LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                  ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-807-992B-9
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US-08-807-992B-12
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US-08-807-992B-12
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 8, 2004, 12:15:17; Search time 13 Seconds (without alignments) 66.594 Million cell updates/sec Run on:

US-09-761-636A-14 52 1 CISVPLVPC 9

Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283366 segs, 96191526 residues Searched:

790 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	MHC H2-L antigen -	glycogen phosphory	118K stomach cance	locustamyotropin I	enamelin f - bovin	tetrameric protein	metallothionein-A	coat protein beta	glycoprotein compo	205K excantigen -	granulocyte-colony	60K Ca binding pro	ofolate	lectin - potato (f	Ξ	T-cell receptor be	flagellar protein	aggrecan - bovine	endoglycosylcerami	major postsynaptic	conopressin S - co	Ig heavy chain CRD	Ig heavy chain CRD	collagen alpha 2(V	R-phycoerythrin al	dnaA protein - Pse	alpha-1,4-glucan-p	hypothetical colla	catch-relaxing pep
	e e	165546	A60521	A60356	A61620	S10783	S66419	151049	S13636	H48394	G33098	154017	PT0080	148105	521288	D48186	PH0943	E42364	842620	B39745	A42689	B28495	PT0247	PT0268	826508	B22565	B34835	B26206	A35039	ECMUCR
	DB	2	7	~	۲3	~	~	7	~	~	7	4	7	~	~	(1	~	~	~	7	~1	7	71	N	7	7	7	7	4	7
	Match Length	9	Ŋ	σ	9	80	σ	4	6	9	œ	œ	6	7	80	6	6	Ŋ	7	80	∞	σ	σ	σ	σ	ഹ	9	9	9	7
*	Match	42.3	36.5	36.5	34.6	7	32.7	٥.	30.8	28.8	28.8	28.8	28.8	26.9	26.9	26.9	26.9	25.0	25.0	25.0	25.0	25.0	25.0	25.0	25.0	3	23.1	23.1	23.1	23.1
	Score	22	19	19	18	17	17	16	16	15	15	15	15	14	14	14	14	13	13	13	13	13	13	13	##	12	12	12	12	12
Regult	No.	-	7	m	4	ഗ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

seed protein ws-5	Ig H chain V-D-J r	T-cell receptor be	hypothetical prote	neutral proteinase	T-cell receptor be	sperm-activating p	kidney and bladder	phosphoenolpyruvat	3',5'-cyclic-GMP p	T-cell receptor be					
E61491	PH1602	PH0932	S16324	A35180	PH0934	S19329	G58502	855696	A53797	PH0935	PH0937	PH0902	PH0917	PH0918	PH0921
7	7	7	~	~	7	~	~	7	7	7	~	7	71	7	73
7	7	7	80	8	00	6	σ	σ	σ	6	σ	σ	σ	σ	σ
23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1	23.1
12	12	12	12	12	12	12	12	12	12	12	12	12	12	17	12
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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0; Gaps
                                                                                                                 Query Match 42.3%; Score 22; DB 2; Length 6; Best Local Similarity 75.0%; Pred. No. 2.8e+05; Matches 3; Conservative 1; Mismatches 0; Indels
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6 LVPC 9 ð 셤

RESULT 2

C'Species: Liza ramada C'Date: 11-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2003 C'Accession: A60521 R'Bonamusa, L.; Baanante, I.V. Comp. Bacoham. Physiol. B 95, 295-301, 1990 A;Title: Purification and characterization of glycogen phosphorylase B from skeletal mu A;Reference number: A60521; MUID:90227907; PMID:2109669 glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment) N.Alternate names: glycogen phosphorylase b

A;Accession: A60521

A;Molecule type: protein
A;Residues: 1-5 < FBONS
C;Superfamily: glucan phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experi

Query Match 36.5%; Score 19; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 4; Conservative 0; Mismatches 0; Indels

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Gaps

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2 ISVP 5 à 셤

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Signedies oncorrynchus mykiss (rainbow trout)
C;Species oncorrynchus mykiss (rainbow trout)
C;Species oncorrynchus mykiss (rainbow trout)
C;Species oncorrynchus mykiss (rainbow trout)
C;Accession: 151049
Expecies oncorrynchus mykiss (rainbow trout (oncorryncus mykiss) myRigisson, P.B.; Kling, P.; Brkell, L.J.; Kille, P.

Bur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (oncorryncus mykiss) myReference number: 151049; MUID:95324545; PMID:7601121
A;Recession: 151049
A;Reterence number: Islo49
A;Recession: 151049
A;Residues: 1-4 <olsp.
A;Residues: 1-4 <ol>p. p. <o
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
R;Serafini, T.; Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orci, L.; Rothman, J.E.; Wiel
Nature 349, 215-220, 1991
Nature 349, 215-220, 1991
A;Title: A coat subunit of Golgl-derived non-clathrin-coated vesicles with homology to A;Reference number: S13656; MUID:91101693; PMID:1898984
       tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment) c;Species: Spinacia oleracea (spinach) c;Species: Spinacia oleracea (spinach) C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997 C;Accession: S66419 R;Kuwabara, T. FBBS Lett. 371, 195-198, 1995 A;File: The 60-KDa precursor to the dithiothreitol-sensitive tetrameric protease of sp: A;Reference number: S66419; MUID:95402209; PMID:7672127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.8%; Score 16; DB 2; Length 4; 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.8%; Score 16; DB 2; Length 9; llarity 50.0%; Pred. No. 2.8e+05; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 17; DB 2; Length 9;
Pred. No. 2.8e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coat protein beta chain, Golgi-derived - rabbit (fragment)
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A;Residues: 1-9 <SEX.
(Superfamily: coatomer complex beta chain
C;Reywords: Golgi apparatus; protein transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metallothionein-A - rainbow trout (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                    32.7%;
50.0%;
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Best Local Similarity 100.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Conservative
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein A;Residues: 1-9 <KUW>
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 2; Conserv
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5 IPIV 8
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2 PILP 5
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C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C;Accession: S1078 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
R;Strawich, B.; Glimcher, M.J.
Bur. J. Blochem. 191, 47-56, 11990
Bur. J. Blochem. 191, 47-56, 11990
A;Atille: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albu A;Reference number: S10780; MUID:90336641; PMID:2379503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A. Insect Biochem. Mol. Biol. 22, 447-452, 1992
A;Title: Isolation, identification and synthesis of locustamyotropin III and IV, two add A;Reference number: A61620
                                                                                                                                                            Int. J. Cancer 45, 783-787, 1990
A;Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A;Reference number: A60356; MUID:90216080; PMID:2323853
A;Accession: A60356
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C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
C;Accession: A61620
118K stomach cancer antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60356
R;Shiraishi, Y.
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <SCH>
C;Reywords: amidated carboxyl end; neuropeptide
F;9/Modified site: amidated carboxyl end (Leu) #status experimental
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Pred. No. 2.8e+05;
1; Mismatches 1; Indels
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34.6%; Score 18; DB 2; L
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1;
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A;Residues: 1-8 <STR>
C;Keywords: enamel; phosphoprotein
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60.0%;
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Best Local Similarity 60.09
Matches 3; Conservative
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A, Residues: 1-9 <SHI>
C, Keywords: glycoprotein
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Best Local Similarity
Matches 3; Conserv
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1 MPLPP 5
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3; Conservative
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <TRE>
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Abote: human gene engineered and expressed in Echerichia coli

C;Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000

C;Accession: 154017

C;Date: D: D: Drumond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.

Gene 65, 13-22, 1988

A;Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac
                                                                            glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr
C;Species: Bos primigenius taurus (cattle)
C;Abte: 19-NOV-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: H48394
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. MOI. Biol. Int. 29, 545-554, 1993
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
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C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: G33098
R;Nichols, J.H.; Hager, L.P.
Rubitred to the Protein Sequence Database, May 1990
A;Reference number: A33098
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A;Accession: I54017
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: maNA
A;Mesidues: 1-8 < DBV)
A;Residues: 1-8 < DBV)
A;Cross-references: GB:M20922; NID:9806638; PIDN:AAA66353.1; PID:9183043
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A;Note: sequence extracted from NCBI backbone (NCBIP:131518)
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                 A; Reference number: A48394; MUID:93250576; PMID:8485470
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A,Molecule type: protein
A,Residues: 1-8 <NIC>
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A;Molecule type: protein
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Best Local Similarity
Matches 3; Conserv
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1 VELLGC 6
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VPL 4
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28.8%; Score 15; DB 4; Length 8; 75.0%; Pred. No. 2.8e+05;

Query Match Best Local Similarity

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Or Ca binding protein - edible frog (fragment)

C,Species: Rana esculenta (edible frog)

C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C,Datesion: Programment

R,Trevesoo, S, Zorzato, F.; Chiozzi, P.; Melandri, P.; Volpe, P.; Pozzan, T.

Biochem. Biophys. Res. Commun. 175, 444-450, 1991

Biochem. Biophys. Res. Commun. 175, 444-450, 1991

A,Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calret

A,Reference number: PT0080; MUID:91207333; PMID:2018493
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C;Species: Cricetulus griseus (Chinese hamster)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 04-569-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Accession: I48105
R;Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.
R;Azizkhan, J.S., 6228-6236, 1986
A;Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihyd
A;Reference number: I48105, MUID: 87776541; PMID: 3047702
A;Accession: I48105
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C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
C;Accession: S21288
R;Millar, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Slabas, A.R.; Bolwell, G.P. Biochem. J. 283, 813-821, 1992
A;Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characterizati A;Reference number: S21288; MUID:92272683; PMID:1590771
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Pred. No. 2.8e+05;
1; Mismatches 0;
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28.8%; Score 15; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0;
1;
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A;Molecule type: DNA
A;Residues: 1-7 <RES>
Mismatches
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A;Residues: 1-8 <MIL>
A;Experimental source: var. Ulster Sceptre
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Typese RI subunit - wood tobacco (fragment)
C;Species: Micoriana sylvestris (wood tobacco)
C;Species: Micoriana sylvestris (wood tobacco)
C;Species: Micoriana sylvestris (wood tobacco)
C;Accession: D48186
R;De Paepe, R.; Forchioni, A.; Cherrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5936, 1993
A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP syntha
A;Reference number: A48186; MuID:93317598; PMID:8327463
A;Accession: D48186
A;Accession: D48186
A;Accession: D48186
A;Accession: D48186
A;Residues: 1-9-CDEI>
A;Residues: 1-9-CDEI>
A;Residues: 1-9-CDEI>
A;Residues: 1-9-CDEI>
A;Rote: sequence extracted from NCBI backbone (NCBIP:134871)
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26.9%; Score 14; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels
Ouery Match 26.9%; Score 14; DB 2; Length 8; Best Local Similarity 50.0%; Pred. No. 2.8e+05; Matches 3; Conservative 0; Mismatches 3; Indels
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(Rel. 41, Created)
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Copyright (c) 1993 - 2004 Compugen Ltd.
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52
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Match Length
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0;
P1741 pichia jadi
P82099 litcria rub
P82100 litcria rub
P13736 mytilus edu
P13737 mytilus edu
P58803 conus imper
P81675 piuns pinas
P35910 achatina fu
P35920 achatina fu
P35921 achatina fu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Methylated-DNA--protein-cysteine methyltransferase (BC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        irreversibly inactivated.
-!- CATALYTIC ACTIVITY: DNA (containing 6-0-methylguanine) +
[protein]-L-cysteine = DNA (without 6-0-methylguanine) + protein
S-methyl-L-cysteine.
-!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
InterPro; IRRO01497; Methyltransf_1.
PROSITE; PS00374; MGMT; PARTIAL.
DNA repair; Transferase, Methyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90174912; PubMed=2308822;
Rydberg B., Hall J., Karran P.;
"Active site amino acid sequence of the bovine O6-methylguanine-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALKYL GROUP ACCEPTOR (BY SIMILARITY).
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Pred. No. 1.4e+05;
0; Mismatches 1; Indels
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                                                               1_MYTED
2_MYTED
P_CONIM
6_PINPS
1_ACHFU
2_ACHFU
3_ACHFU
    TAL3 PICJA
E103 LITRU
E104 LITRU
CIP1 MYTED
                                                                                                                                                                                                    ACT CARMA
AKH LIBAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methyltransferase.";
Nucleic Acids Res. 18:17-21(1990).
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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BRHP
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Best Local Similarity 75.0%,
.-heg 3; Conservative
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PRT;

9 A

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    J. Comp. Neurol. 419:352-363(2000).
    -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic

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                                                                                                                                                                                                                                                                                                                                                             Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C., Banchez J.-C., James R., Tissot J.-D., Bjellqvist B., Hochstrasser D.F.;

"Plasma protein map: an update by microsequencing.";

Blectrophoresis 13:707-714(1992).

-!- MISCELLANBRONS: On the 2D-gel the determined pI of this unknown protein is: 4.6, its MM is: 46 kDa.

SWISS-2DPAGE; P30089; HUMAN.
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE—Corpora cardiaca;
MEDLINE=97333923; PubMed=9210163;
Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
Isolation and structural elucidation of two pyrokinins from the retrocerebral complex of the American cockroach.";
Peptides 18:473-478(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amotation update)
Pyrokinin-2 (Pea-Pk-2) (FXPRL-amide).
Pyrokinin-2 (Pea-Pk-2) (FXPRL-amide).
Enkalyota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattaria; Blattoidea; NSBL_TANID=6978;
                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; DB 1; Length 9;
Pred. No. 1.4e+05;
0; Mismatches 1; Indel8
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-!- TISSUE SPECIFICITY: Corpora cardiaca.
-!- MASS SPECTROMETRY: WM-883; METHOD-MALDI.
-!- SIMILARITY: Belongs to the pyrokinin family.
-- InterPro; IPRO01484; Pyrokinin.
-- PROSITE; PS00539; PYROKININ; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        419:352-363 (2000)
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93092937; PubMed=1459097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                    STANDARD;
                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISSUE SPECIFICITY.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 PLPP 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PLVP 8
                                                                                                                                                                                                                                                                                                                                     TISSUE=Plasma;
                                                  UPA3 HUMAN P30089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PERAM
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                 JPA3 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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            RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                      Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                 "A novel D-leucine-containing Conus peptide: diverse conformational dynamics in the contryphan family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
.
                                 Bukaryota; Metazoa; Molinsca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 1; Length 9;
Pred. No. 1.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 18; DB 1; Length 8; Pred. No. 1.4e+05; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                 J. Pept. Res. 54:93-99(1999).

-! SUBCELIULAR LOCATION. Secreted.

-! TISSUE SPECIFICITY: Expressed by the venom duct.

-! ALISSUE SPECIFICITY: Expressed by the venom duct.

-! MASS SPECIFICITY: Expressed by the venom duct.

-! MASS SPECIFICITY: BW-888.4; METHOD=LSIMS.

-! SIMILARITY: Belongs to the contryphan family.

TOXID: Hydroxylation; D-amino acid.

DISULIFIED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 4 D-LEUCINE.
8 AA; 890 MW; 75A367672732CEB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (myotropic activity).
-!- SIMILARITY: Belongs to the pyrokinin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA.
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                                                                                                                                      [1]
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
STRAIN-Clipperton Island; TISSUB-Venom;
MEDLINE-99388839; PubMed=10461743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Locustamyotropin 3 (LOM-MT-3).
Locusta migratoria (Migratory locust).
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                   Conus purpurascens (Purple cone)
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75.0%;
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Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A61620; A61620.
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CVLLP 6
                                                                                                              NCBI TaxID=41690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PLVP 8
.eu-contryphan-P.
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                                                                                                                                                                                                                                                     Olivera B.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=104895;
                                                                                                                                                                                                                                                                                                                                                                                                               6 LVP 8
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SEQUENCE
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UNSÜRE
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P82096;
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  SETTER CC REFERENCE SO SETTER SO SET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the American cockroach.";
J. Comp. Neurol. 419:352-363(2000).
-!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..
G
                                                                                                                               Gaps
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MEDILNE-20189894; PubMed=10723010;
Predel R., Eckert M.;
"Tagma-specific distribution of PXPRLamides in the nervous system of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Retrocerebral complex, MEDLINE-99212469; PubMed=10196736; Professor Retrocerebral complex, Predel R., Kallner R., Nachman R.J., Holman G.M., Rapus J., Gaede "Differential distribution of pyrokinin-isoforms in cerebral and abdominal neurohemal organs of the American cockroach."; Insect Biochem. Mol. Biol. 29:139-144(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Periplaneta americana (American cockroach).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.8%; Score 15; DB 1; Length 8; 100.0%; Pred. No. 1.4e+05; attive 0; Mismatches 0; Indels
                                                                               h Similarity 50.0%; Pred. No. 1.4e+05; 3; Conservative 0; Mismatches 3; Indels
Neuropeptide, Amidation; Pyrokinin.

MOD RES

8

AMIDATION.
SEQÜENCE 8 AA, 884 MW; C834176DD9D7775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 8 AMIDATION.
8 AA; 997 MW; 0B34177409D772C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
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                                                                                                                                                                                                                                                                                                                           8 AA.
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Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blattidae, Periplaneta.
NCBL_TaxID=6978;
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                                                                                                        Local Similarity
                                                                                                                                                                          3 SVPLVP 8
                                                                                                                                                                                                                SPPFAP 6
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P30093;
                                                                                                                                                                                                                                                                                                                           PPK3 PERAM
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                                                                                      Query Match
                                                                                                                                                                                                                                                                                  RESULT 6
PPK3_PERAM
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                                                                                                          Best Loca
Matches
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Gaps
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MEDLINE-93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C., Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.R.;
"Plasma protein map: an update by microsequencing.";
Blectrophoresis 13:707-714(1992).
-I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.05, its MW is: 37 kDa.
SWISS-2DPAGE; P30093; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Litoria rubella (Desert tree frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
Pelodryadinae; Litoria.
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Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=6493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.0%; Score 13; DB 1; Length 6; Best Local Similarity 66.7%; Pred. No. 1.4e+05; Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                         28.8%; Score 15; DB 1; Length 9; 100.0%; Pred. No. 1.4e+05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       9 AA; 1042 MW; SC14477AEB0772C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;
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01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aust. J. Chem. 52:639-645 (1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Andation.
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Query Match
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8 AA.

PRT;

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STANDARD;
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Matches 2; Conserv
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SEQUENCE
    CYDPO
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SEQUENCE
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P81010;
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          MEDLINE-88058932; PubMed-3680228;
Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Olivera B.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Catch-relaxing peptide (CARP).
Mytilus edulis (Ble mussel).
Bukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                               "Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms."; J. Biol. Chem. 262:15821-15824(1987).
                                                                                                       MEDLINE=89024586; PubMed=3052286;
A Gray W.R., Olivera B.M., Cruz L.J.;
The peptide toxins from venomous Couns snails.";
Annu. Rev. Biochem. 57:665-700(1988).
C. 1- FUNCTION: Targete vasopressin-oxytocin related receptors.
C. 1- TISSUE SPECIFICITY: Expressed by the venom duct.
C. 1- SINGELLULAR LOCATION: Secreted.
C. 1- SINGELLULAR LY: Belongs to the vasopressin/oxytocin family.
PIR: B28495; B28495.
R InterPro; IPR000981; Neurhyp_horm.
R Pfam; PR00220; hormone4; 1.
R PROSTIE: PS00226; NGROMPOPHYS_HORM; 1.
R PROSTIE: PAMADATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Carch-relaxing peptide isolated from Mytilus pedal ganglia.";
Brain Res. 422:374-376(1987)
-!- FUNCTION: This peptide exhibits both potentiating (contract and inhibitory (relaxation) effects on the anterior byssus retractor muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.1%; Score 12; DB 1; Length 7; 20.0%; Pred. No. 1.4e+05; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   11 mm, -
25.0%; Score 13; DB 1; Length >;
'^^ Ok; Pred. No. 1.4e+05; Indels
                                                                                                                                                                                                                                                                 9 9 AMIDATION.
9 AA; 1031 MW; 17EB176EB4540050 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA; 831 MW; 6734072687669DB0 CRC64;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA.
                                                                                                                                                                                                                                                                                                                ilarity 100.0%; Pred. No. 1.4
Conservative 0; Mismatches
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Hormone; Amidation.
MOD RES 7
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Matches 2; Conserv
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Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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15-UUL-1998 (Rel. 36, Last sequence update)
16-UUL-1998 (Rel. 42, Last annotation update)
Allergen Fus s 1596* (Fragment)
Pusarium solani (subsp. pisi) (Nectria haematococca).
Busaryora, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetiade; Hypocreales; Nectriaceae; Nectria.
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                                                                   Cydia pomonella (Codling moth).

Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Boytera, Emopterygota; Lepidoptera; Glossata; Ditrysia;

Tortricoidea; Tortricidae; Olethreutinae; Cydia.
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01-APR-1993 (Rel. 25, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 12; DB 1; Length 8; Pred. No. 1.4e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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submitted (JUL-1997) to Swiss-Prot.
-1-ALLERGEN: Causes an allergic reaction in human.
                                                                                                                                                                                                                                                                                                                                                                         Peptides 18:1301-1309(1997).
-1- SIMILARITY: Belongs to the allatostatin family.
Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA; 898 MW; C372C441F5B69041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 8 AMIDATION.
8 AA; 936 MW; 0B2879C45B573767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.1%; Score 12; DB 1; I 66.7%; Pred. No. 1.4e+05; iive 1; Mismatches 0;
30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Cydiastatin 6.
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STRAIN=IARI 3596, IISSUE=Mycelium;
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Best Local Similarity
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UPA.I HUMAN
AC P30087;
DT 01-APR-1993
DT 15-APR-2094
DE UNKNOWN procte
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RESULT 11

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completed: March 8, 2004, 12:18:24
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                                                     (Fragment).
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                                                                                                              "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-!- MISCELLANBOUS: On the 2D-gel the determined pI of this unknown
protein is: 4.9, its MW is: 65 kDa.
SWISS-2DPAGE; P30087; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoldea;
Penaeidae; Penaeus.
NCBI_TaxID=6687;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                             TISSURE-Plasma;
MEDLINE-93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hoobstrasser D.F.,
                                                                                                                                                                                                                23.1%; Score 12; DB 1; Length 8; 66.7%; Pred. No. 1.4e+05; ive 1; Mismatches 0; Indels
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GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
                                                                                                                                                                                                                                                                                                                                             28-722.)
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Penaeus monodon (Penoeid shrimp)

        MOD_RES
        9
        AMIDATION.

        SEQUENCE
        9 AA, 1106 MW; B60B07340735A766 CRC64;

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Pred. No. 1.4e+05;
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66.7%;
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Best Local Similarity
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5 NVP 7
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FLA2_TREHY
ID FLA2_TREHY
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FARS_PENMO
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Koopman M.B.H. Baates E., van Vorstenbosch C.J.A.H.V.,
van der Zeijst B.A.M., Kusters J.G.;
J. Gen. Microbiol. 138:2697-2706(1992).
-!- FUNCTION: Component of the outer layer of the flagella.
-!- FUNCTION: Component of the outer layer of the flagella.
SHEATH PROTEINS, FLAAI (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
THAT CONTAINS THREE PROTEINS FLABI (37 kDa), FLABS (34 kDa) AND
                                                                                                                                                                                                      Treponema hyodysenteriae (Serpulina hyodysenteriae).
Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Flagellar filament outer layer protein flaA2 (35 kDa sheath protein)
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Pred. No. 1.4e+05;
1; Mismatches 0; Indels
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-!- SUBCELLULAR LOCATION: Periplasmic flagellum.
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C5;
MEDLINE=93139764; PubMed=1487733;
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2; Conservative
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March 8, 2004, 12:14:57; Search time 34.5 Seconds (without alignments) 82.309 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1: sp_archea:*
2: sp_archea:*
3: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
11: sp_rodent:*
2: sp_virus:*
3: sp_virus:*
4: sp_unclassified:*
5: sp_virus:*
6: sp_virus:*
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Gapop 10.0 , Gapext 0.5
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1 CISVPLVPC 9
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	O9p8e5 kluvveromyc	042564 fugu rubrip	Q56140 streptococc	Q8ay15 carassius a	Q8aum7 carassius a	Q7x6a3 zea mays su	P93233 lycopersico	002831 oryctolagus	Q9try3 sus sp. ins	Q16220 homo sapien	Q9umf3 homo sapien	Q8qvd3 ovine respi	Q07624 rous sarcom	078225 mus musculu	Q988j8 oryza sativ	O35953 mus musculu
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MEDLINE=95047254; PubMed=7958782;
Constable 4., Mollet B.;
"Isolation and characterisation of promoter regions from Streptococcus
                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-97442476; PubMed-9295353;
Plummer N.W., McBurney M.W., Meißler M.H.;
Plummer N.W., McBurney M.W., Meißler M.H.;
"Alternative splicing of the sodium channel SCNBA predicts a truncated two-domain protein in feral brain and non-neuronal cells.";
J. Biol. Chem. 272:24008-24015(1997).
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                                   Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Tetraodontidae; Takifugu.
NCBI_TaxID=31033;
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Truncated voltage-gated sodium channel alpha subunit (Fragment).
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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7 AA; 730 MW; 75B72EA2C73772A0 CRC64;
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FEMS Microbiol. Lett. 122:85-90(1994).
EMBL; X78210; CAA55045.1; -.
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Tchoudakova N.V., Kishida M., Wood E., Callard G.V.;
Tchouder characteristics of two CYP19 genes differentially expressed in the brain and ovary of teleost fish.";
J. Steroid Biochem. Mol. Biol. 0:0-0(2001).
EMBL, 3P324995; AAN32616.1;
EMBL, AF324996; AAN32616.1;
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                                                                                                                                                                                                       Tchoudakova A.V., Kishida M., Wood E., Callard G.V.; "Promoter characteristics of two CYP19 genes differentially expressed in the brain and ovary of teleost fish.";
                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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BMBL; AF324897; AAN32618.1; -.
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Shimasaki S., Gao L., Shimonaka M., Ling N.; Isolation and molecular cloning of insulin-like growth factor-binding protein-6.";
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"Bridence for insufficient chondrocytic differentiation during repair
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"Bridence for insufficient chondrocytic differentiation during repair
Matrix Biol. 15:39-47(1996).

EMBL; S83371; AAD14433.1;
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MEDLINE-94320083; PubMed=8044796;
Magalla S.R., Spindel E.R.; F.R.; F. Flanking region of the human gastrin-
Functional analysis of the 5'-flanking region of the human gastrin-
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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01.-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.-MAY-2002 (TrEMBLrel. 11, Last senotation update)
101.-MU-2002 (TrEMBLrel. 21, Last annotation update)
Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
                                                      MEDLINE=96377339; PubMed=8783186;
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
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SEQÜENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;
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NCBI_TaxID=9986;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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                                                  STRAIN-cv. 38-11, and cv. A632; Wilson L.M., Whitt S.R., Ibanez A.M., Rocheford T.R., Goodman M.M., Buckler E.S. IV.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97351561; PubMed-9207843; Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.; Discortial induction of seven 1-aminocyolopropane-1-carboxylate synthase genes by elicitor in suspension cultures of tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 24, Last sequence update)
Pro alpha 1 type III collagen protein (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria, Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                           32.7%; Score 17; DB 10; Length 9; 66.7%; Pred. No. 1e+06; cive 1; Mismatches 0; Indels
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WHAY-1997 (TrEMBLrel. 03, Last sequence update)
01-UMA-0997 (TrEMBLrel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
                                                                                                                   "Dissection of maize starch production by candidate gene association.";
                                                                                                                                                         Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY290305; AAP45331.1; -.
EMBL; AY290311; AAP45337.1; -.
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7 AA; 828 MW; 71B412C7377415D0 CRC64;
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Plant Mol. Biol. 34:275-286(1997).
EMBL; U75692; AAC49682.1; -
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5 LPC 7
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MEDLINE=93010967; PubMed=1327749;
DODIZE O., Spahr P.F.; PubMed=1327749;

BODIZE O., Spahr P.F.; Parish of France of Rous sarcoma virus leader RNA in translation and genome packaging.";
EMBO J. 11:3747-3757(1952).

EMBD: X67569; CAA47862.1; -7 SEQUENCE 7 AA, 672 MW; 776045A7687DD6F0 CRC64;
                                                                 30.8%; Score 16; DB 12; Length 9; 100.0%; Pred. No. 1e+06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Rous sarcoma virus (strain Prague C).
Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
VCBL_TaxID=11888;
                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1996 (TEMBLrel. 01, Last sequence update)
01-MAR-2003 (TEMBLrel. 23, Last annotation update)
       9 9 AA; 1154 MW; 8B6A3EA764541415 CRC64;
                                                                                         Local Similarity 100.
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"The human PD-1 gene: complete cDNA, genomic organization, and developmentally regulated expression in B cell progenitors.";
Gene 197:177-187(1997).
EMBL, U64864, AACS1774.1;
NON_TER
releasing peptide gene in small cell lung carcinoma cell lines."; Cancer Res. 54:4461-4467(1994).

EMBL; S73265; AAD14116.1; -.
GO; GO:0005654; C:nucleus; NAS.
GO; GO:0006555; P:regulation of transcription, DNA-dependent; NAS.
NON TER. 9 9 9
SEQÜENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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BLOADLINE-2180659; PubMed=11724134;
Bleraky N.Z., Kania S.A., Potgieter L.N.;

"The ovine respiratory syncytial virus F gene sequence and its diagnostic application.";

J. vet. Diagn. Invest. 13:455-461(2001).

EMBL; AF334398; AAL91343.1; -.
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Yituses; ssRvA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=28869;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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MEDLINE=97473511; PubMed=9332365;
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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STRAIN=CRO435; TISSUB=Kidney;
MEDLINE=88084418; PubMed=3692165;
MEDLINE=88084418; PubMed=3692165;
RGolubic M., Budimir O., Schoepfer R., Kasahara M., Mayer W.E.,
Figueroa F., Klein J.;
"Nucleotide sequence analysis of class II genes borne by mouse t
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               28.8%; Score 15; DB 15; Length 7; 50.0%; Pred. No. 1e+06; ive 1; Mismatches 1; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                            9 AA.
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EMBL; L38589; AAA57293.1; -.
Query Match
Best Local Similarity 50.0%;
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geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* geneseqp1990s:* geneseqp2004s:* Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

seq length: 0 seq length: 9

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aau04533 VEGF base	4		~		Aay84998 Amino aci		Aay63242 Protocadh	4	Aam24655 Human MHC	Abq35050 Endostati		Aay84999 Amino aci		Aay03909 Hepatitis			Aau94456 Human nov	Aau94653 Human nov	Adc44488 Endotheli	_	Aaw85926 Rodent IL	Abp99702 Human sec		Aau04530 VEGF base
SUMMARIES	AAU04533	ABG35134	ABB46931	ABG60522	ABR56920	AAY84998	ADC44293	AAY63242	AAE07204	AAM24655	ABG35050	AAR95843	AAY84999	ADC44308	AAY03909	AAP10098	ABP21743	AAU94456	AAU94653	ADC44488	ADC59359	AAW85926	ABP99702	AAB64710	AAU04530
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* Query Match	100.0	51.9	51.9	51.9	51.9	50.0	50.0	50.0		50.0	50.0	48.1	48.1	48.1	46.2	46.2	46.2	46.2	46.2	46.2	46.2	44.2	44.2	44.2	44.2
Score	52	27	27	27	27	26	26	26	26	26	26	25	25	25	24	24	24	24	24	24	24	23	23	23	23
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Aar58417 Partial p	Aar58416 Partial p	Aar58415 Partial p	Aar58418 Partial p	Aaw99327 Human IgG	Aay10322 T cell ep	Aaw99853 HIV-1 gpl	Aay47758 Immunogen	Aay45765 Immunogen	Aay45766 Immunogen	Aay48998 Membrane	Aay51358 MHC type	Aab36017 Human bet	Aab27093 Plasmodiu	Aab61826 Human 19	Aae26894 Linker pe	Abg35060 Angiostat	Abq35128 Pancreati	Abg60516 Selective	Abg80004 MHC class
AAR58417	AAR58416	AAR58415	AAR58418	AAW99327	AAY10322	AAW99853	AAY47758	AAY45765	AAY45766	AAY48998	AAY51358	AAB36017	AAB27093	AAB61826	AAE26894	ABG35060	ABG35128	ABG60516	ABG80004
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44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2
23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23	23
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Human, VEGF; vascular endothelial growth factor; angiogenesis; neovascularisation; lymphangiogenesis; psoriasis; tumour; diabetes induced neovascular sequelae; rheumatoid arthritis; diabetic retinopathy; chronic inflammation; cyclic. VEGF based monocyclic peptide 11. AAU04533 standard; peptide; 9 AA. (first entry) 26-SEP-2001 AAU04533; RESULT 1

Synthetic.

 ..9 /note= "This bond cyclises the peptide" Location/Qualifiers Key Disulfide-bond WO200152875-A1 26-JUL-2001.

18-JAN-2000; 2000US-0176293P. 16-MAY-2000; 2000US-0204590P. 18-JAN-2001; 2001WO-US001533

Cendron A; Stacker S, (LUDW-) LUDWIG INST CANCER RES. Hughes RA, Achen MG,

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

Claim 49; Page 32; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the expose loop of human VBGPD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring betabet acarbon separation distances on opposite antiparallel strands of a

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peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptides with at least one amino acid deleted prior to cyclisation are used to interfere with angiogenesis, comprising monocyclic characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, contain, vabstance-induced malignant or benigh tumour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascular sation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, or chronic liver infection. The peptides are also used to modulate vascular permeability in a mammal (the mammal has a condition characterised by fluid accumulation in peripheral limbs or in lungs, peritoneal cavity, pieura, or brain. The peptides are used to induced by VBGF-C or D and accumulation with an analyse are used to interfere with at least one biological activity induced by VBGF-V VBGF-C or D and are also used in combination with an anti-inflammatory agent, to treat a struction in the peripherally theumatoid arthritis, psoriasis and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Targeting peptide, cancer, Hodgkin's disease, cytostatic; immunosuppressive; anti-inflammatory; antiarthritic; antiviral; antiatherosclerotic; antidabetic; antibacterial; diabetes mellitus; inflammatory disease, arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     diabetic retinopathy
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Best Local Similarity
Matches 9; Conserv
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Claim 56; Page 288; 298pp; English.

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This invention relates to a novel method for identifying disease targeting peptides. The method comprises exposing a sample from an organ, tissue or cell type of interest, to a phage display library and recovering phage bound to the sample (the phage expresses targeting recovering phage bound to the sample (the phage expresses targeting peptides). The peptides identified by the method of the invention may anti-display to anti-diametric, anti-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive; cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft; organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprising a desmosomal cacherin cell adhesion recognition CAR sequence (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cacherin CAR sequence, a substance such as an antibody or antigen-binding fragment that specifically binds a desmosomal cacherin CAR sequence and/or a polymucleotide encoching a polypeptide that comprises a desmosomal cacherin CAR sequence or analogue. The modulating agents have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating agents for inhibiting or enhancing desmosomal cadherin mediated cell adhesion, useful for facilitating wound healing and/or reducing scar tissue, treating cancer and inducing apoptosis.
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Pred. No. 1.4e+06;
1; Mismatches 3; Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 targeting peptide of the invention
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Best Local Similarity
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The invention relates to an isolated peptide of 100 amino acids or less in size useful for targeting delivery to an organ or tissue, particularly to the training a disease, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial inflection, viral infection, cardiovascular disease or degenerative disease. The peptide is also useful for inducing apoptosis, particularly to a subject with ischaemia, cancer, arthritis, diabetes, candiovascular disease, inflammation or macular degeneration. Furthermore, the peptide is useful for diagnosing the diseases cited above. Targeting peptides of the invention can also be used to deliver an agent to a foetus, by attaching a peptide to the agent and administering the peptide to a pregnant subject. Sequences ABG60126-ABG60574 represent selective targeting peptides of the invention
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antiapoptotic activity and are used to
                           facilitate wound healing and/or reduce scar tissue, for enhancing adhesion of foreign tissue implants (e.g. skin graft or organ implant), treating an autoimmune blistering disorder and to treat cancer (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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   immunosuppressive, cytostatic and
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17-JAN-2001; 2001US-00765101.
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                                                                                                                                                                                                                                                                                                                            44.48;
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Matches 4; Conserv
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Sequence 9 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        also be used for targeting delivery to an organ or tissue, such as placental delivery. A receptor that binds to a placenta targeting peptide is used to screen compounds for teratogenic activity. ABR56806 to ABR56927 and ACC79106 to ACC79111 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for treating obesity or a lipodystropathy, which comprises: (a) obtaining a targeting peptide selective for adipose tissue; (b) attaching the peptide to a therapeutic agent to form a complex; (c) administering the complex to a subject; and (d) inducing weight loss in the subject or treating lipodystropathy. The adipose targeting peptides have anorectic and antilipsemic activities, and can be used in peptide and gene therapy. The method is used for treating obesity or a lipodystropathy that is related to infection with human immunodeficiency virus (HIV). The peptides used in the method can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating obesity or a lipodystropathy comprises obtaining a targeting peptide selective for adipose tissue, attaching the peptide to a therapeutic agent to form a complex, and administering the complex to a
                                                                                                                                                                                                                                                                                                                               Targeting peptide; obesity; lipodystropathy; anorectic; antilipaemic; peptide therapy; gene therapy; infection; human immunodeficiency virus; HIV; placental dellvery; teratogenic; placenta; adipose; pancreatic; beta-3 integrin; beta-5 integrin; spleen; aminopeptidase A.
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Length 9;
Score 27; DB 5; I
Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                Pancreatic targeting peptide SEQ ID NO:137.
                                  1; Mismatches
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                                                                                                                                                                                             ABR56920 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001; 2001WO-US027692
51.9%;
55.6%;
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Query Match
Best Local Similarity 55.69
Matches 5, Conservative
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                                                                                          |:| | | CMSSPGVAC 9
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                                                                     1 CISVPLVPC
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus.
                                                                                                                                                                                                                                                               30-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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endothelial cell binding protein; ECBP; anti-tumour; cytostatic;
vasotropic; antipsoriatic; dermatological; ophthalmological;
antidiabetic; antiarthritic; vulnerary; antiulcer; antiinflammatory;

antibacterial; gynaecological; angiogenesis.

Endothelial cell binding peptide SEQ ID NO:21.

(first entry)

18-DEC-2003

ADC44293;

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The present sequence represents an endothelial cell-binding peptide motif. The peptide may be identified using the method of the invention.

The specification describes a method for generating a peptide having a calected biological activity. The method comprises displaying the selected biological activity. The method comprises displaying the peptide display library. The method comprises displaying the correct of a genetic display package for those containing peptides which have population display packages for those containing peptides which have containing peptides which have a selection of peptides waying effects on cell proliferation.

Conferentiation, death and migration, as well as in the identification of peptides which have anti-proliferative activity with respect to one or corrective peptides (e.g. which are active as anti-fungal or anti-infective peptides (e.g. which are active as anti-fungal or anti-infective peptides (e.g. which are active as anti-fungal or anti-infectival), receptor protein effectors, and ligands for orphan receptors contained the contained may be used to test currently interactions for cell currently and channels interactions for cell
                                                                                                                                                                                          Endothelial cell-binding peptide, Genetic display package; peptide display library; affinity selection, population display package; cell proliferation, cell differentiation, cell dath; cell migration; angiogenic activity; infective peptide; anti-fungal; anti-bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generating a peptide with a selected biological activity useful for identifying endothelial inhibitors and peptides with anti-angiogenic activity by combining peptide display libraries in a display and a
                                                                                                                                                      Amino acid sequence of an endothelial cell-binding peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 3; Length 7;
Pred. No. 1.4e+06;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 42; 86pp; English.
                                     AAY84998 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00174943.
                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US024276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%;
                                                                                                                   21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                         receptor protein effector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gyuris J, Morris AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-339649/29.
                                                                                                                                                                                                                                                                                                                                                           WO200023465-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secretion mode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-0CT-1998;
                                                                                                                                                                                                                                                                                                                   Inidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                      19-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-2000.
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                                                                           AAY84998;
RESULT 6
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Novel synthetic or recombinant polypeptide useful for promoting, reducir proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.

Claim 3; SEQ ID NO 21; 126pp; English.

Tsaioun K;

Morris AJ,

Lamphere L,

Gyuris J,

WPI; 2003-482072/45.

(GPCB-) GPC BIOTECH INC.

01-NOV-2002; 2002WO-US035258. 01-NOV-2001; 2001US-0334822P

WO2003037172-A2.

Synthetic.

08-MAY-2003.

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tumour, cytostatic, vasotropic, antipsoriatic, dermatological, cumour, cytostatic, vasotropic, antipsoriatic, dermatological, antidiabetic, antiarthritic, vulnerary, antiulcer, antiantemarcy, antibacterial, and gynaecological activity. The peptide is useful for promoting, reducing the proliferation and/or migration of endothelial cells, by treating the cells with an ECBP agonist, which is preferably the peptide, to promote proliferation and/or migration of the treated cells, and for reducing or promoting angiogenesis, by treating the cells with an ECBP antagonist, which is preferably the peptide of the invention is preferably the peptide of the invention and or applied of the invention and or general section and or more steel to ECBP antagonist. Which is suffered for manufacturing a medicament for promote or reduce angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing angiogenesis. ECBP sequences are useful to alter the infectivity spectrum of a viral particle. The present sequence represents an ECBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell binding protein (BCBP) sequences. A peptide of the invention has anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 26; DB 7; Length 7; 66.7%; Pred. No. 1.4e+06; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY63242 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 SVPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::||||
2 AIPLVP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Gaps

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Similarity 66.7 4; Conservative

Local

Best Loc Matches

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::||||| 2 AIPLVP 7 3 SVPLVP 8

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ADC44293 standard; peptide; 7 AA.

ADC44293 ID ADC4 RESULT 7

Colostrinin, nootropic, neuroprotective, immunomodulatory, antibacterial, Parkinson's disease; Alzheimer's disease; mental disorder; food additive; central nervous system disorder, neurodegenerative disorder; weight loss; beta-amyloid plaque; psychosis, neurosis, cachexia, motor neuron disease; acquired immunological deficiency; neurological disorder; dementia;

Modified colostrinin cyclic peptide #10.

(first entry)

06-NOV-2001

AAE07204;

AAE07204 standard; peptide; 9 AA.

/note= "N-terminal acetyl; this residue forms a cyclic linkage with Ser found at the C-terminal end"

WO200155199-A1

02-AUG-2001.

Location/Qualifiers

Key Modified-site

antiviral; cyclic.

Synthetic.

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comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating nonclassical cadherin cell adhesion recognition (CAR) sequence. The MAs can be used for modulating conclassical cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting usual palogenesis in a mammal, inhibiting of treating obesity in a mammal, stimulating corresping cells, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age cor reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age creducing can also be used for treating e.g. psoriasis, arthritis, age related macular degeneration, multiple sclerosis and diabetes. The AXX6652 to AAX6652 represent specifically claimed peptides, and have the contract of the contract of the contract of the contraction and diagnosis and in bioreactors. AXX6652 to AAX6652 represent sequences used in
             Modulation, nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; DB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin; cadherin-16; T-cadherin; pB-cadherin; protocadherin; desmocollin; calcium binding; cancer; tumour; obesity; rheumatoid athhitis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cadherin modulating agents, used for modulating nonclassical cadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes cadherin modulating agents (MA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the exemplification of the present invention
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 84; Page 201; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00187859.
99US-00234395.
99US-00264516.
                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-CA000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00073040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gour BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-038791/03.
                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3laschuk OW,
                                                                                                                                                                                                                                                                                                                                          WO9957149-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-1998;
20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1999;
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                                                                                                                                                                                                            Synthetic
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                                                                                                                                               50.0%; Score 26; DB 3; Length 9; 44.4%; Pred. No. 1.4e+06; ive 2; Mismatches 3; Indel8
                                                                                                                                                  ilarity 44.4%;
Conservative
                                                                                                                                                  Best Local Similarity Matches 4; Conserv
                                                                                                                                                Query Match
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The invention relates to colostrinin peptide fragments which are useful, inter alia, in the treatment of chronic disorders of the immune system colostrinin peptides are used as a medicament in the treatment of neurological disorders e.g., dementia, neurodegenerative disorders e.g., Alzheimer's disease, motor neuron disease e.g., Parkinson's disease, mental disorders e.g., psychosis and neurosis, in acquired immunological deficiencies, chronic bacterial and viral infections and diseases characterised by the presence of beta-awyloid plaques and as a distary supplement for babies, mall children, adults and senile persons, who have been subjected to chemotherapy or have suffered from cachexia or weight loss due to the chronic disease. Colostrinin peptides are also used as food additives and as an auxillary withdrawal treatment for drug addicts, after a period of detoxification and in persons dependent on stimulants. Colostrinin peptides and to treat emotional disturbances, e.g. emotional colostrinin peptides improves the development of immune system in a new benefit equence is modified colostrinin cyclic peptide #10 related to the child and to correct the immunological deficiencies in a child. The present equations are made of the immunological deficiencies in a child. The characteries and the development of immune system in a new construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 AA;
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Peptide useful as an interalia in the treatment of e.g. disorders of the immune system and the central nervous system comprises ten amino-terminal amino acid sequence derived from peptides present in colostrinin.

(REGE-) REGEN THERAPEUTICS PLC. 26-JAN-2000; 2000GB-00001825. 26-JAN-2001; 2001WO-GB000329.

WPI; 2001-488775/53.

Georgiades JA;

Example 2; Page 9; 40pp; English.

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Gaps ; 0

1 CISVPLV 7

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| :: || | 1 CFALDLVTC 9

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1 CISVPLVPC

Targeting peptide; cancer; Hodgkin's disease; cytostatic; immunosuppressive; anti-inflammatory; antiarthritic; antiviral; antiathreoscleroric; antidabetic; antidabetic; disbetes mellitus; inflammatory disease; arthritis; atherosclerosis; cancer; autoimmune disease; bacterial infection; viral infection.

Endostatin targeting peptide #49.

(first entry)

15-JUL-2002

ABG35050;

a

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The polypeptide sequences represent the 83P5G4-related protein and peptide fragments of the protein. 83P5G4 exhibits prostate specific peptide fragments of the protein. 83P5G4 exhibits prostate specific peptide fragments of the prostate, bladder, kidney, brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum, con and lung. The 83P5G4 polynucleotide, its related protein and peptide fragments and specific PCR primars are therefore useful for diagnosing and treating cancer. A vector comprising a polynucleotide which encodes a single chain monoclonal antibody, that immunospecifically binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a polynucleotide having the 83P5G4 coding sequence, are both useful in the preparation of a composition for treating a patient with a cancer that capresses 83P5G4. The sequences can be used in diagnostic methods to monitor the level of 83P5G4 gene products in serum, blood, urine and to thereby detect the presence of cancerous cells
                                                                                                                                                                        83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; tumour; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix; single chain monoclonal antibody; urine; uterus; rectum; stomach; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An isolated 83P5G4-related protein useful as a diagnostic and/or
therapeutic agent in multiple cancers such as prostate, bladder and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                     Human MHC class I molecule HLA-A2 binding 83P5G4 peptide #32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 4; Length 9;
Pred. No. 1.4e+06;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Faris M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Challita-Bid PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; Page 77; 112pp; English.
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ID ABG35050 standard; peptide; 9 AA.
                              AAM24655 standard; peptide; 9 AA
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                                                                                                                                                                                                                                                                                                                                                                                                  09-FEB-2001; 2001WO-US004426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Afar DEH, Chal:
, Jakobovits A;
                                                                                                         04-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 50.0 hes 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UROG-) UROGENESYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :|| ||
LPLPLRPC 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514669/56.
                                                                                                                                                                                                                                                      chromosome 1q31-q32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                             WO200159115-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hubert RS, A
                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                L6-AUG-2001
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Best Local Si
Matches 4;
                                                                    AAM24655;
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RESULT 10
                     AAM2465
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Identifying targeting peptides useful for treating e.g. diabetes mellitus, inflammatory diseases, cancer, or autoimmune diseases, comprises exposing a sample to a phage display library and recovering phage bound to the sample.

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101. 07-SEP-2001; 2001WO-US027702.

WO200220722-A2.

14-MAR-2002.

Unidentified.

(TEXA) UNIV TEXAS SYSTEM

Pasqualini R;

Arap W,

WPI; 2002-383050/41.

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This invention relates to a novel method for identifying disease targeting peptides. The method comprises exposing a sample from an organ, tissue or cell type of interest, to a phage display library and recovering phage bound to the sample (the phage expresses targeting opepides). The peptides identified by the method of the invention may nate cytostatic, immunosuppressive, anti-inflammatory, antiarthritic, antidiabetic, antidiametery, antiarthritic, antidiabetic, antidiametery and antiviral cativities. The methods and composition are useful for identifying activities and one or more receptors for a targeting peptide. The targeting peptides and one or more receptors for a targeting peptide. The targeting peptides and one or more receptors for a targeting peptide. The targeting peptide way also be used for selective delivery of therapeutic agents, including gene therapy vectors and fusion proteins, to specific organs, tissues, or cell types in subject. The targeting peptide may also be used for treating diseases such as diabetes mellitus, inflammatory diseases, carbitits, atherosclerosis, cancer, autoimmune diseases, bacterial and viral infections and Hodgkin's disease. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 26; DB 5; I 55.6%; Pred. No. 1.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 56; Page 252; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   targeting peptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR95843 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CISVPLVPC 9
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Best Local Similarity
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27-APR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC44308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
ADC44308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR95832-R95844 represent the altered fragments of the insulin-like growth factor-1 (IGF-1) muteins of the invention. This sequence represents the N-terminal residues 63-67 of the IGF-1 mutein C67. The wild type IGF-1 sequence is represented by AAR87744. These muteins contain a non-native cystein residue substituted for one of the first (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             last) four amino acid residues of this sequence. Polyethylene glycol (PEG) conjugates are then created from the muteins, where the PEG is attached to the non-native cystein residue. The PEG is attached to the face cystein through an activating group selected from maleimide, sulphydryl, thiol, triflate, tresylate, aziride, exirane or 5-pyridyl. The conjugates can also comprise a second polypeptide attached to the PEG. The conjugates may be used for the treatment of IGF associated conditions, such as dwarfism, diabetes, periodontal disease or osteoprosis. Advantages associated with these conjugates are that they have a higher molecular weight, and an extended circulating half life in comparison to wild type IGF.
                           Insulin-like growth factor-1; IGF-1; polyethylene glycol; PEG; triflate; PF1/PEG conjugate; maleimide; sulphydryl; thiol; tresylate; aziride; exirane; 5-pyridyl; therapy; dwarfism; diabetes; periodontal disease; osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endothelial cell-binding peptide, Genetic display package,
peptide display library; affinity selection; population display package;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conjugates for treatment of, e.g. dwarfism, diabetes, or osteoporosis comprising polyethylene glycol attached to mutein of IGF at free
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of an endothelial cell-binding peptide motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 2; Length 5;
Pred. No. 1.4e+06;
0; Mismatches 1; Indels
                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.1%; Scc.
80.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 22; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY84999 standard; peptide; 5 AA.
IGF-1 mutein C67 residues 63-67.
                                                                                                                                                                                                                                                                                95WO-US006540.
                                                                                                                                                                                 /note= "A5C"
                                                                                                                                                                                                                                                                                                                                                (AMGE-) AMGEN BOULDER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Mcdermott MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-020360/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLVPC 9
                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PLKPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5 AA;
                                                                                                                                                                                                                                                                              24-MAY-1995;
                                                                                                                                                                                                                                                                                                               24-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-2000
                                                                                                                                                                                                                WO9532003-A1
                                                                                                                                                                                                                                               30-NOV-1995
                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY84999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cysteine
                                                                                                                                                                                                                                                                                                                                                                                 Cox GN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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motif. The peptide may be identified using the method of the invention. The presult sequence represents an endouterating a peptide having a relected biological activity. The method comprises displaying the selected biological activity. The method comprises displaying the peptides on the outer surface of a genetic display package to create a peptide display library, and using affinity selection to enrich the population display packages for those containing peptides which have desired specificity to the target cell. The method may be used in the selection of peptides having effects on cell proliferation, differentiation, death and migration, as well as in the identification of peptides which have anti-proliferative activity with respect to one or more types of cells, peptides with (anti-) angiogenic activity, anti-infective peptides which are active as anti-fungal or anti-infective peptides which are active as anti-fungal or anti-infective peptides which are active as anti-fungal or anti-infective peptides which are active more types of cells, peptides which are active and ligands for orphan receptors for which no ligand is known. Moreover, the method may be used to test functional ligand-receptor or ligand-ion channel interactions for cell surface-localized receptors and channels
cell proliferation; cell differentiation; cell death; cell migration; angiogenic activity; infective peptide; anti-fungal; anti-bacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generating a peptide with a selected biological activity useful for identifying endothelial inhibitors and peptides with anti-angiogenic activity by combining peptide display libraries in a display and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endothelial cell binding protein; ECBP; anti-tumour; cytostatic; vasotropic; antipsoriatic; dermatological; ophthalmological; antiathritic; vulnerary; antiulcer; antiathritic; vulnerary; antiulcer; antiinflammatory; antibacterial; gynaecological; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents an endothelial cell-binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endothelial cell binding peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 42; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC44308 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US024276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00174943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.1%;
80.0%;
                                                                                         receptor protein effector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gyuris J, Morris AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MITO-) MITOTIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-339649/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VPLVP 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||||
1 IPLVP
                                                                                                                                                                                                                                                         WO200023465-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secretion mode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5 AA;
                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-OCT-1998;
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Job time : 50.5 secs
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Best Local Similarity
Matches 4, Conserv
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                                                                                                                                                                                                                                                                                                  The invention relates to a novel isolated, synthetic or recombinant peptide or polypeptide which includes one or more endothelial cell peptide or polypeptide which includes one or more endothelial cell cell binding protein (EGBP) sequences. A peptide of the invention has anticumour, cytostatic, vasotropic, antipsoriatic, dermatological, ophthalmological, antidiabetic, antiarthritic, vulnerary, antiulcer, antimidramatory, antidiabetic, antiarthritic, vulnerary, antiulcer, antidiamatory, antidiapetic, antiarthritic, vulnerary, antiulcer, antidiamatory, antidiapetic, antiarthritic, vulnerary, antiulcer, antidiamatory, tedicing the proliferation and/or migration of is useful for promoting the cells with an EGBP antagoniet, which is preferably the peptide, to promote proliferation and/or migration of the created cells, and for reducing or promoting angiogenesis, by treating an endicament for promote or reduce angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing a are useful for promoting or reduce angiogenesis at one or more sites in a treated mammal. The medicament is useful for promoting or reducing an angiogenesis. ECBP sequences are useful to alter the infectivity spectrum of a viral particle. The present sequence represents an ECBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                             Novel synthetic or recombinant polypeptide useful for promoting, reducing proliferation and/or migration of endothelial cells, and for modulating angiogenesis, has endothelial cell binding protein sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C; inhibitor; NS3 protease; NS4A cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25; DB 7; L
Pred. No. 1.4e+06;
1; Mismatches 0;
                                                                                                                                                     Tsaioun K;
                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 36; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                     Gyuris J, Lamphere L, Morris AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "N-Ac-Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY03909 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C inhibitor peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-CA000765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.1%;
80.0%;
                                                              01-NOV-2002; 2002WO-US035258.
                                                                                         01-NOV-2001; 2001US-0334822P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Conservative
                                                                                                                        (GPCB-) GPC BIOTECH INC.
                                                                                                                                                                                WPI; 2003-482072/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 4; Conserv
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WO2003037172-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-1998;
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                                08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY03909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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New generically described peptides are disclosed which are NS3 protease inhibitors useful for treating hepatitis C virus (HCV) infection. The present sequence represents a specific example of these peptides. In a test to determine inhibition in a NS3 protease/NS4A cofactor peptide radiometric assay, this peptide had an IC50 value of 92 micromolar
                                                                                                                   Tsantrizos Y;
                                                                                                                                                                                                                                                                          σţ
                                                                                                                                                                                                                                                                          New peptides inhibitors of NS3 protease - useful for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A 46.2%; Score 24; DB 2; Length 6; Similarity 100.0%; Pred. No. 1.4e+06; 4; Conservative 0; Mismatches 0; Indels
                                                                                                                      Simoneau B,
                                                                                                                      Rancourt J,
                                                         (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 108; 158pp; English.
                                                                                                                      Poupart M,
97US-0055186P.
                                                                                                                                                                                                                                                                                                          hepatitis C infections
                                                                                                                                                                                                             WPI; 1999-167361/14.
                                                                                                                         Llinas-Brunet M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6 AA;
   11-AUG-1997;
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Gaps

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(without alignments)
73.092 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/FUSNATA.PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                                                                                                                                                                                           March 8, 2004, 12:19:53; Search time 26 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809742 seqs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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52
1 CISVPLVPC 9
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 14, Appl	Sequence 11221, A	Sequence 11228, A	Sequence 11250, A		Sequence 11258, A	Sequence 11259, A	Sequence 11265, A	Sequence 11275, A	Sequence 11280, A	Sequence 21, Appl	Sequence 148, App	Sequence 2726, Ap	Sequence 2726, Ap	Sequence 36, Appl
CHINGING		ID De	US-09-761-636A-14	US-10-154-884B-11221	US-10-154-884B-11228	US-10-154-884B-11250	US-10-154-884B-11254	US-10-154-884B-11258	US-10-154-884B-11259	US-10-154-884B-11265	US-10-154-884B-11275	US-10-154-884B-11280	US-10-286-457-21	US-09-780-053-148	US-10-006-869-2726	US-10-395-032-2726	US-10-286-457-36
		BB	- 6	12	15	15	15	15	15	15	15	15	14	σ	14	15	14
		Query Match Length DB		Q	9	σ	6	9	σ	9	9	6	7	9	9	6	. 2
	₩	Query Match	100.0	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	51.9	50.0	50.0	50.0	50.0	48.1
		Score	52	27	27	27	27	27	27	27	27	27	26	26	26	26	25
		Result No.	1		m	4	5	9	7	80	6	10	11	12	13	14	15

Sequence 52, Appl	6	Sequence 636, App	Sequence 216, App	Sequence 90, Appl	4	~		Sequence 123, App		ò		Sequence 69, Appl	_	Seguence 68, Appl		Sequence 68, Appl	Sequence 116, App	Seguence 67, Appl	Seguence 115, App	Sequence 2, Appli	Sequence 67, Appl	Sequence 115, App	Sequence 114, App	Sequence 114, App	Sequence 113, App	Sequence 113, App	Sequence 39, Appl	Sequence 74, Appl	Sequence 39, Appl
US-10-428-335-52	US-09-932-165-439	US-09-932-165-636	US-10-286-457-216	US-10-428-335-90	US-09-761-636A-11	US-09-997-579-19	US-10-038-407-29	US-10-254-446A-123	US-10-286-457-165	US-10-286-457-500	US-10-164-279-15	US-09-947-387-69	US-10-138-375-69	US-09-947-387-68	US-09-947-387-116	US-10-138-375-68	US-10-138-375-116	US-09-947-387-67	US-09-947-387-115	US-10-010-184A-2	US-10-138-375-67	US-10-138-375-115	US-09-947-387-114	US-10-138-375-114	US-09-947-387-113	US-10-138-375-113	US-09-918-243-39	US-09-918-243-74	US-09-905-083-39
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47.1	46.2	46.2	46.2	46.2	44.2	44.2	44.2	44.2	44.2	44.2	44.2	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3	42.3
24.5	24	24	24	24	23	23	23	23	23	23	23	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22	22
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

DD I CISYPLVFC 9 RESULT 2 US-10-154-884B-11221 ; Publication No. US/20040005561A1

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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Manion, Jane
APPLICANT: Manion, Jane
APPLICANT: Manchion, Jane
APPLICANT: March W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Owners: US 60/10/154,804B
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-04-28
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-04-28
PRIOR PIL
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PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR PILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: US 60/202,084

PRIOR PILING DATE: 2000-05-04

PRIOR PLING DATE: 2000-05-22

PRIOR APPLICATION NUMBER: US 60/218,950

PRIOR PILING DATE: 2000-07-14

PRIOR PILING DATE: 2000-07-14

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR PILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 11290

SOFTWARE: PASLERQ for Windows Version 3.0

SOFTWARE: PASLERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.9%; Score 27; DB 15; Length 9; 66.7%; Pred. No. 7.2e+05; Live 2; Mismatches 0; Indels
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Best Local Similarity 66.77
Matches 4; Conservative
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US-10-154-884B-11250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Homo sapiens
US-10-154-884B-11228
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                                                                                                               APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Andate, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Lematological Malignancies
FILE REFERENCE: 014058-0135210S
CURRENT FILING DATE: 2000-01-05-23
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APLICATION NUMBER: US 60/200,545
PRIOR APLICATION NUMBER: US 60/200,739
PRIOR FILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR PILING DATE: 2000-05-20
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR PILING DATE: 2000-05-20
PRIOR PILING DATE: 2000-05-20
PRIOR PILING DATE: 2000-05-20
PRIOR PILING DATE: 2000-05-20
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR PILING DATE: 2000-07-14
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Publication No. US20040005561A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICANT: Adjate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hamalological Malignancies
FILE REFERENCE: 014058-013521US
CURRENT FILING DATE: 2002-05-23
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    See File Wrapper or PALM.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: US 60/190,479
PRIOR PELING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR PELING DATE: 2000-04-27
PRIOR PELING DATE: 2000-04-27
PRIOR PELING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
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NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 66.77
- Thes 4; Conservative
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ORGANISM: Homo sapiens
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2 CLSVPV 7
                                                   GENERAL INFORMATION:
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US-10-154-884B-11228
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APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Theraj
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PILING DATE: 2000-03-27
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
                                                                THIN KAPKENCE: 01408-01352.01

FILIN KAPKENCE: 01408-01352.01

CURRENT FILING DATE: 2002-05-23

FRIOR APPLICATION NUMBER: US 60/196,126

FRIOR APPLICATION NUMBER: US 60/190,479

FRIOR FILING DATE: 2000-03-01

FRIOR FILING DATE: 2000-03-01

FRIOR FILING DATE: 2000-04-27

FRIOR FILING DATE: 2000-04-28

FRIOR FILING DATE: 2000-04-28

FRIOR FILING DATE: 2000-04-28

FRIOR FILING DATE: 2000-04-28

FRIOR FILING DATE: 2000-05-04

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3 OF INVENTION: Hematological Malignancies REFERENCE: 014058-013521US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 4; Conservative
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US-10-154-884B-11258
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4 CLSVPV 9
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TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-
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APPLICANN: Algate, Paul A.
APPLICANN: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
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Score 27; DB 15; Length 9;
Pred. No. 7.2e+05;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11254, Application US/10154884B Publication No. US20040005561A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Wall A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: COTIXA COTPORATION
    51.9%;
66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                          4; Conservative
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    Query Match
Best Local Similarity
Matches 4; Conserv
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CLSVPV 9
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US-10-154-884B-11258
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APPLICANT: Galger, Alexander
APPLICANT: Galger, Alexander
APPLICANT: Galger, Alexander
APPLICANT: Adjate, Paul A.
APPLICANT: Galger, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Macrawith March Macrawith Mannion, Jane
APPLICANT: Corixa Corporations and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Hematological Malignancies
FILE REPERENTE: 2000-03-01
FRICKENT FILING DATE: 2000-03-01
FRICK PALING DATE: 2000-04-28
FRICK FILING DATE: 2000-05-01
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Mar.
APPLICANT: Retter, Mar.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01351108
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
                                                                                                                                              Sequence 11275, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
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US-10-154-884B-11275
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Best Local Similarity
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                                                                                     RESULT 9
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TITLE OF INVENTION: Hematological Malignancies
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CURRENT APPLICATION NUMBER: US/10/154,884B

CURRENT APPLICATION NUMBER: US/00/154,884B

CURRENT APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-04-29

PRIOR FILING DATE: 2000-04-27

PRIOR PILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28

PRIOR PLILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-07-14

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PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-09-03
PRIOR FILING APPLICATION NUMBER: US 60/222,903
PRIOR FILING DAPICATION data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11259
LENGTH: 9
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Pred. No. 7.2e+05;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
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66.7%;
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Best Local Similarity 66.7
Matches 4; Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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; ORGANISM: Homo sapiens
US-10-154-884B-11265
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US-10-154-884B-11259
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APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Symonds, James Matthew
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REPERENCE: 100086.4077.
CURRENT APPLICATION NUMBER: US/10/006,869
CURRENT FILING DATE: 2001-12-03
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PATENTIN Ver. 2.0
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Publication No. US20030229199A1
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Grounds, James Matthew
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
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                                                                                    APPLICANT: Elafa Levin
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
APPLICANT: Aya Jaxobovita
APPLICANT: Aya Jaxobovita
TITLE OF INVENTION: 819E5G4: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER;
FILE REPERRENCE: 129.515G11
CURRENT APPLICATION NUMBER: US/09/780,053
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/181,261
PRIOR APPLICATION NUMBER: 60/181,261
NUMBER OF SEQ ID NOS: 716
SOFTWARE: FREUESC for Windows Version 4.0
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   Daniel E.H. Afar
Pia M. Challita-Eid
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ORGANISM: Artificial Sequence
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ORGANISM: Homo Sapiens
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Best Local Similarity
Matches 4; Conservat
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2 LPLPLRPC 9
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US~10-006-869-2726
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US-10-395-032-2726
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   APPLICANT:
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APPLICANT:
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Publication No. US2030166004A1
GENERAL INFORMATION:
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
ITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REPERENCE: GPC1-P01-110
CURRENT APPLICATION NUMBER: US/10/286,457
CURRENT FILING DATE: 2002-11-01
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
SEQ ID NOS: 684
SEQ ID NO 21
LENGTH: 7
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                PRIOR PLING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR PLING DATE: 2000-04-28
PRIOR PLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR PLING DATE: 2000-06-28
PRIOR PLING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-03
PRIOR PLING DATE: 2000-05-04
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FILING DATE: 2000-03-17
APPLICATION NUMBER: US 60/200,545
FILING DATE: 2000-04-27
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GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
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ORGANISM: Artificial Sequence
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Beet Local Similarity 66.74;
Thes 4; Conservative
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US-10-154-884B-11280
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Best Local Similarity
Matches 4; Conserv
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2 AIPLVP 7
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4 CLSVPV 9
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US-09-780-053-148
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US-10-286-457-21
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TYPE: PRT

CRGANISM: Artificial Sequence

FRATURE:

CTHER INFORMATION: artificial sequence isolated from random peptide libraries, based

CTHER INFORMATION: ability to selectively bind to endothelial cells

US-10-286-457-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-10-286-457-36
Sequence 36, Application US/10286457
Sequence 36, Application US/10286457
Publication No. US20030166004A1
GENERAL INFORMATION:
APPLICANT: USKO GYURLS et al.
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
TITLE NO FUNCANTION: UNDER: US/10/286,457
CURRENT FALIAND BATE: 2002-11-01
PRIOR PELICATION NUMBER: 60/3348022
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-01
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PatentIn version 3.1
LENGTH: 5
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                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
PEATON: REALISM: Artificial Sequence
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-10-395-032-2726
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 48.1%; Score 25; DB 14; Length 5; Best Local Similarity 80.0%; Pred. No. 7.2e+05; Matches 4; Conservative 1; Mismatches 0; Indels
FILE REFERENCE: 100086.407C9
CURRENT PELLICHION NUMBER: US/10/395,032
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 4052
SEQ ID NO 2726
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: March 8, 2004, 12:28:23
Job time : 27 secs
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1 CFALDLVTC 9
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1 IPLVP 5
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 8, 2004, 11:41:37 ; Search time 20 Seconds
(without alignments)
110.620 Million cell updates/sec Run on:

US-09-761-636A-4 133 1 QGQHIGEMSFLQHNKCECRPKKD 23 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 seqs, 96191526 residues Searched:

4494 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 23

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ch Length DB ID 23 2 B38671 23 2 B36671 23 2 B90596 23 2 B90596 23 2 B90596 23 2 B60565 24 22 1 MXKN3 25 22 2 H66433 26 23 2 AF0533 27 2 B33882 28 23 2 AF0533 29 2 AF0533 20 2 B33882 20 2 B33882 20 2 B33882 20 2 B33882 20 2 B60365 20 2 B33882 20 2 B60365 20 2 B60365 21 2 A33883 22 2 A7207 23 2 A59048 23 12 2 A72318 24 2 B33883 25 2 B60365 26 2 B60365 27 2 B33882 28 2 B60365 29 2 B60365 20 2 B60365 20 2 B60365 21 2 A32601 22 A32601 23 12 2 A32601 24 2 B33883 25 2 B60365 26 2 B60365 27 2 B33883 28 2 B60365 29 2 B60365 20 2 B60365																														
Score Match Length DB 33 24.8 23.2 26 19.5 22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Description		homeodomain protei	probable transcrip	protein T17H7.9 [i	small hypothetical	mu-conotoxin GIIIA	mu-conotoxin GIIIB	antibiotic GE2270				cadmium-binding pe	cadmium-binding he	protein QF200070 -	metallothionein I	dentinal fluid tra	chymotrypsin inhib	T-cell receptor J-	convulsant peptide	alpha-2-macroglobu	caerulein-like pep	hypothetical 1.4K		tubulin beta chain	polistes mastopara	interferon alpha r	zinc finger protei	translation initia	T cell receptor be
Score March Length 33 24.8 33 24.8 33 24.8 25.5 19.2 25.5 19.2 25.5 19.2 25.5 19.2 25.6 19.5 25.6 19.5 25.7 19.2 25.8 18.8 24.8 18.0 24.5 18.0 24.5 18.0 24.5 18.0 24.5 18.0 24.18.0 24.18.0 24.18.0 25.17.3 23.5 17.3 23.5 17.3 23.5 17.3 23.5 17.3 23.17.3 23.17.3 23.17.3 23.17.3 24.18.0 25.2 25.2 26.2 27.3 28.3 28.3 29.3 29.3 29.3 20.3 20.3 20.3 20.3 20.3 20.3 20.3 20	ID	B38671	860565	B90996	H86433	T37096	MXKN1	MXKN2	A61210	S23637	AF0535	MXXXN3	A33882	B33882	PA0104	A31252	DIRT	B60365	S47207	A59048	866636	A13687	JQ2308	JQ2318	S39413	OMWAPP	S41601	D45193	JN0264	S57520
25.5 19.2 24.8 18.0 24.1 1	ch DB	23 2	23 2	22 2	22 2	19 2	22 1	22 1	13 2	23 2	23 2	22 1	2	7 2	14 2	19 2	20 2	20 2	21 2	23 2	9	10 2	12 2	12 2	13 2	14 1	14 2	16 2	16 2	18 2
Score 25.55 26.55	Leng			••	• •	. ,	•••					•••					••	••	••											
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T-cell receptor be H+-transporting tw metallothionein is	gonadoliberin - se hypothetical prote corticostatic pept	1-cell receptor al geed storage prote T-cell receptor al casein kinase II (T-cell receptor be T-cell receptor be integrase homolog	gene RB1 protein - shikimate 5-dehydr theta defensin-1 -
D49404 PC7072 S59622	RHLMGS T46794 JH0460	FH0/99 PA0015 PH1443 A45133	E49255 F49039 E40442	I78870 I40062 C59089
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ALIGNMENTS

alpha-am

Gaps 5; Query Match 24.8%; Score 33; DB 2; Length 23; Best Local Similarity 46.7%; Pred. No. 1.6e+02; Matches 7; Conservative 1; Mismatches 5; Indels Length 23;

ij.

8 MSFLQHNKC--ECRP 20 8 ISFTQKKKCVKHCNP 22 q à

RESULT 2

homeodomain protein hrox3 - California red abalone (fragment)
C;Species: Haliotis rufescens (California red abalone)
C;Species: Haliotis rufescens (California red abalone)
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999
C;Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 15-Oct-1999
R;Pegnan, B.M.; Morse, D.E.
Mol. Marine Biol. Biotechnol. 2, 1-9, 1993
MyTitle: Identification of eight homeobox-containing transcripts expressed during larvant A;Reference number: S60564; MUID:93372986; PMID:7689904

A,Molecule type: mRNA A,Residues: 1-23 <DEG> A,Cross-references: EMBL:X79372; NID:g495110; PIDN:CAA55917.1; PID:g495111

A;Gene: hrox3 C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

C; Genetics:

Query Match 23.3%; Score 31; DB 2; Length 23; Best Local Similarity 55.6%; Pred. No. 3.3e+02; Matches 5; Conservative 2; Mismatches 2; Indels 2 NKYLCRPRR 10 14 NKCECRPKK 22 **8** 8

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Gaps

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Gaps

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Length 19;

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Risato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.
FEBS Lett. 155, 277-280, 1983
A;Title: The amino acid sequences of homologous hydroxyproline-containing myotoxins fro
A;Reference number: A91309; MUID:83210170; PMID:6852238
A;Accession: A01786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
B;Molecule 1-22 cART>
R;Cruz, L.J; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydl
B;Cruz, L.J; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydl
A;Title: Couns geographus toxins that discriminate between neuronal and muscle sodium c
A;Title: Couns geographus toxins that discriminate between neuronal and muscle sodium c
A;Attle: A25579; MUID:85261316; PMID:2410412
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21588
A;Accession: T37096
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-19 <500.
A;Cross-references: EMBL:AL109950; PIDN:CAB52947.1; GSPDB:GN00070; SCOEDB:SCJ4.13c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mu-conotoxin GIIIA [validated] - cone shell (Conus geographus)
N;Alternate names: geographutoxin I (GTX I); myotoxin I
C;Species: Conus geographus (geography cone)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                  h Similarity 33.3%; Pred. No. 2e+03; Length 1 Similarity 33.3%; Pred. No. 2e+03; 5; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 HIGEMSFLQHNKCEC 18
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Best Local Similarity
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A;Gene: SCOEDB:SCJ4.13c
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H86433
C;Accession: H86433
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., J.J., J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: Add analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: H86433
A;Accession: H86433
A;Accession: H86433
A;Residues: 1-22 <STO>
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                                                                                                                                                                       C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: B90996
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc
A;Reference number: 899629; MUID:21156231; PMID:11288796
                                                                                                                                                  probable transcription regulator (imported) - Escherichia coli (strain O157:H7, substrai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o'
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A;Experimental source: strain 0157:H7, substrain RIMD 0509952
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T37096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 19.5%; Score 26; DB 2; L Similarity 37.5%; Pred. No. 1.9e+03; 6; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.5%; Score 26; DB 2; L
50.0%; Pred. No. 1.9e+03;
Live 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 IGEMSFLQHNKCECRP 20
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Best Local Similarity
Matches 6; Conserva'
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Matches 5; Conserv
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A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Molecule type: procein
A, Residues: 1.22 CRUb
R, Kohda, D:, Lancelin, J.M.; Inagaki, F.; Wakamatsu, K.
B, Kohda, D:, Lancelin, J.M.; Molos, Conformation by (1) H-NMR, residues 1-22
A, Reference number: A51994; PDB:1TCG
A, Contence: annotation; Conformation by (1) H-NMR, residues 1-22
A, Contence: annotation; Conformation GIIIA in aqueous solution.
A, Pitla: Tertiary structure of contoxin GIIIA in aqueous solution.
A, Pitla: Tertiary structure of contoxin GIIIA in aqueous solution.
A, Pitla: Tertiary structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geome R, Ott. K. H.; Becker, S. Gordon, R.D.; Rueterjans, H.
R, Ott. K. H.; Becker, S. Gordon, R.D.; Rueterjans, H.
R, Pitla: Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geome A, Pitla: Solution structure of mu-conotoxin GIIIA analysed by 2D-NMR and distance geome A, Peference number: A58581; MUID:93112275; PMID:1991506
A, Contents: annotation; conformation by (1) H-NMR
R; Wakamatsu, K.; Kohda, D.; Hatanaka, H.; Lancelin, J.M.; Ishida, Y.; Oya, M.; Nakamuri B, A, Title: Structure-activity relationships of mu-conotoxin GIIIA: structure determination A, Reference number: A44244; MUID:93112589; PMID:1335283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: mu-conotoxin
C;Keywords: amidated carboxyl end; hydroxyproline; myotoxin; sodium channel inhibitor;
F;3-15,4-20;10-27/Disulfide bonds: #status experimental
F;6,7/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;12/Modified site: 4-hydroxyproline (Pro) #status experimental
F;22/Modified site: amidated carboxyl end (Ala) #status experimental
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C,Accession: AF0535
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche J.; Woule, S.; O'Gaora, P. (Zroin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0535
A;Accession: AF0535
A;Accession: AF0535
A;Redidues: 1-23 < PAR>
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**Huber, C. f, Klobeck, H.G., Zachau, H.G.

Bur, J. Immunol. 22, 1561-1565, 1992

A, Title: Ongoing V(kappa) - J(kappa) recombination after formation of a productive V(kap
A, Reference number: $23637; MuID: 92289816; PMID: 1601042
A, Accession: $23637
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C;Species: Conus geographus (geography cone)
C;Date: 31-Mar-1989 #sequence_revision 04-Nov-1994 #text_change 23-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
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                                        (Pro) #status experimental
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F:11-12/Cross-link: 2-oxazoline (Cys-Ser) #status experimental F:13/Modified site: amidated carboxyl end (Pro) #status experi
                                                                                               18.8%; Score 25; DB 2; Length 13; 60.0%; Pred. No. 1.7e+03; ive 1; Mismatches 1; Indels
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Pred. No. 2.8e+03;
2; Mismatches 3; Indels
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Pred. No. 2.8e+03;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                        3; Conservative
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Best Local Similarity 46.2
Matches 6; Conservative
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                                                                                                                               Best Local Similarity
Matches 3; Conserv
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9 CKCSP 13
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A; Residues: 1-23 < HUB>
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MXKN3
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A,Residues: 1-22 <SAT>
A,Residues: 1-22 <SAT>
A,Residues: 1-22 <SAT>
B,Chuz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydlo J. Biol. Chem. 260, 9380-9288, 1985
A,Title: Conus geographus toxins that discriminate between neuronal and muscle sodium changement A,Reference number: A23579; MUID:85261316; PMID:2410412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Molecule type: protein
A, Residues: 1-22 < ckUv)
A, Residues: 1-22 < ckUv)
R; Hill, J.M.; Alewood, P.F.; Craik, D.J.
Bubmitted to the Brookhaven Protein Data Bank, April 1996
A, Reference number: A65705, PDB:1GIB
A, Reference number: A65705, PDB:1GIB
A, Rothernts: annotation; conformation by (1) H-NMR, residues 1-22
R; Hill, J.M.; Alewood, P.F.; Craik, D.J.
Biochemistry 35, 8824-8835, 1996
Biochemistry 35, 8824-8835, 1996
A; Title: Three-dimensional solution and solution and solution by (1) H-NMR
A, Reference number: A85890, Mulb:9628040; PMID:8688418
A; Contents: annotation; conformation by (1) H-NMR
                                                                                                                                                                                                                                                                                                                                            R;Sato, S.; Nakamura, H.; Ohizumi, Y.; Kobayashi, J.; Hirata, Y.
PEBB Lett. 155, 277-280, 1983
A;Fitle: The amino acid sequences of homologous hydroxyproline-containing myotoxins from A;Reference number: A91309; MUID:83210170; PMID:6852238
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A. Antibiot. 44, 702-715, 1991
A.fitle: Antibiotic GE2270 A. a novel inhibitor of bacterial protein synthesis. II. Stru
A;Reference number: A61210, MUID:91249090; PMID:1880060
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A;Status: preliminary
A;McMecule type: procein
A;McMecule type: procein
A;McMecule type: procein
A;McMecule type: procein
A;McMecule type: procein
A;McMecule type: procein
F;1-10/Cross-link: thiazole amino end (Cys-Lys) (by 10-C6) #status experimental
F;2-3/Cross-link: 5-methylthiazole (Wal-Cys) #status experimental
F;4-Mcdified site: N4-methylapazagine (Asn) #status experimental
F;7-8/Cross-link: thiazole (Phe-Cys) #status experimental
F;7-8/Cross-link: thiazole (Cys-Cys) #status experimental
F;8-9/Cross-link: pyridine (Cys-Lys) #status experimental
F;9-10/Cross-link: pyridine (Cys-Lys) #status experimental
F;10-11/Cross-link: thiazole (Lys-Cys) #status experimental
F;10-11/Cross-link: thiazole (Lys-Cys) #status experimental
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C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 15-Sep-2000
C;Accession: A01787; B23579
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C;Date: 13-May-1994 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
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Pred. No. 2.3e+03;
2; Mismatches 1; Indels
                                                                                                                                                                    mu-conotoxin GIIIB [validated] - cone shell (Conus geographus)
N/Alternate names: geographutoxin II (GTX II); myotoxin II
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   9 KCKDROCKPOR 19
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Query Match
Best Local Similarity 60.00,
Best Aconservative
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A;Molecule type: protein
Residues: 1-19 <MEH>
C;Superfamily: metallothionein
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Job time: 21 secs
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Best Local Similarity
Matches 4; Conserv
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                                                                 A;Title: Comus geographus toxins that discriminate between neuronal and muscle sodium characteristic comus geographus toxins that discriminate between neuronal and muscle sodium characteristic comus geographus toxins that the procession: C23579
A;Accession: C23579
A;Molecule type: protein
A;Residues: 1-22 <CRU5
C;Superfamily: mu-conotoxin
C;Superfamily: mu-conotoxin
C;Superfamily: mu-conotoxin
C;Superfamily: mu-conotoxin
C;Superfamily: mu-conotoxin
C;3-15,4-20,10-21/plsulfide bonds: #status predicted
F;3-15,4-20,10-21/plsulfide bonds: #status predicted
F;6,7,17/Modified site: 4-hydroxyproline (Pro) #status experimental
F;22/Modified site: amidated carboxyl end (Ala) #status experimental
                 R;Cruz, L.J.; Gray, W.R.; Olivera, B.M.; Zeikus, R.D.; Kerr, L.; Yoshikami, D.; Moczydld
J. Biol. Chem. 260, 9280-9288, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cadmium-binding heptapeptide - downy thornapple
Cispecies: Datura innoxia (downy thornapple)
Cispecies: Datura innoxia (downy thornapple)
Cipate: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
Ciackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A;Title: Poly(gamma-glutamylcysteinyl)glychie: its role in cadmium resistance in plant
A;Reference number: A94182; MUID:88016144; PMID:3477793
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Rjackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Rjackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
A;Title: Poly(gamma-glutamyleysteinyl)glyoine: its role in cadmium resistance in plant A;Reference number: A94182; MUD:88016144; PMID:3477793
A;Molecule type: protein
A;Residues: 1-5 cJAC>
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C,Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
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C,Species: Fusarium sporotrichioides
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Pred. No. 2.8e+05;
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A;Molecule type: protein
A;Residues: 1-7 <JA2>
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Matches 3; Conserv
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C;Accession: C23579
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0104
E;Chow, L.P.; Fakeya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JPID, October 1994
A;Description: Two dimensional polyacrylamide gel electropheresis of Fusarium sporotric
A;Reference number: PA0051
A;Accession: PA0104
A;Accession: PA0104
A;Residues: 1-14 <CHO>
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C;Accession: A31252
R;Mehra, R.K.; Tarbet, E.B.; Gray, W.R.; Winge, D.R.
Proc. Natl. Acad. Sci. U.S.A. 88; 8811-8819, 1988
A;Title: Metal-specific synthesis of two metallothioneins and gamma-glutamyl peptides
A;Reference number: A94212; MUID:89057829; PMID:3194392 C;Species: Candida glabrata C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-Sep-1993 metallothionein I - yeast (Candida glabrata) (fragment)

Gaps ö 18.0%; Score 24; DB 2; Length 19; 60.0%; Pred. No. 3.4e+03; ive 1; Mismatches 1; Indels 60.08;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:*

Database :

		Description	P82299 homa	P01523 conus geogr	P01524 conus geogr	P80924 staphylococ		P05482 conus geogr	P07448 rattus norv	P58845 conus texti	P01517 polistes ja		P04378 petromyzon	P31144 homo sapien	P13211 atractampis	P83243 tityus camb			Q56251 tomato big		P56249 litoria inf	P80904 methanobact	P30254 manduca sex	P01202 equus cabal			Q9twr5 phoneutria								P30426 bothrops in
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RESULT 2

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T = 1-JUL-1986 (Rel. 01, Created)

D = 21-JUL-1986 (Rel. 01, Last sequence update)

D = 28-E8-2003 (Rel. 41, Last amontation update)

D = 28-E8-2003 (Rel. 41, Last amontation update)

D = 28-E8-2003 (Rel. 41, Last amontation update)

D = 28-E8-2003 (Rel. 41, Last amontation update)

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-1- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium channel (VSSC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=83210170; PubMed=6852238; Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.; Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.; mithe amino acid sequences of homologous hydroxyproline-containing mycloxins from the marine snail Conus geographus venom."; FEBS Lett. 155:277-280(1983).
                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
MEDLINE-85261316; PubMed=2410412;
MEDLINE-85261316; PubMed=2410412;
MEDLINE-85261316; PubMed=2410412;
Yoshikami D., Mczydlowski E.;
"Conus geographus toxins that discriminate between neuronal and muscle sodium channels.";
"Biol. Chem. 260:9280-9288 (1985).
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                  21-JUL-1986 (Rel. 01, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Mu-conotoxin GIIIB (Myotoxin II) (Geographutoxin II) (GTx-II).
Comus geographus (Geography cone).
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STRUCTURE BY NMR.
MEDLINE=96280640; PubMed=8688418;
Hill J.M., Alewood P.F., Craik D.J.;
"Three-dimensional solution structure of mu-conotoxin GIIIB, specific blocker of skeletal muscle sodium channels.";
Biochemistry 35:8824-8835 (1996).
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Lancelin J.-M., Kohda D., Tate S.-I., Yanagawa Y., Abe T., Satake M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Tertiary structure of conotoxin GIIA in aqueous solution.";
Biochemistry 30:6908-6916(1991).
-!- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simonishi Y.; "Disulfide pairings in geographutoxin I, a peptide neurotoxin from "Disulfide pairings
                                                                                                                                                                                                                                                                                MEDINE-B3210170; PubMed-6852238; Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.; Sato S., Nakamura H., Ohizumi Y., Kobayashi J., Hirata Y.; "The amino acid sequences of homologous hydroxyproline-containing myotoxins from the marine snail Conus geographus venom."; FEBS Lett. 155:277-280(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91122275; PubMed-1991506; Ott K.-H., Becker S., Gordon R.D., Rueterjans H.; Solution structure of mu-conotoxin GIIIA analysed by 2D-NWR and distance geometry calculations."; FEBS Lett. 278:160-166(1991).
                                                                                                           MEDLINE=85261316; PubMed=2410412; Caixus R.D., Kerr L., CALX L.,. Gray W.R., Olivera B.M., Zeikus R.D., Kerr L., Yoshikami D., Moczydlowski E.; "Conus geographus toxins that discriminate between neuronal and
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25.5; DB 1; Length 22; Pred. No. 5.9e+02; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF05374; Mu-conotoxin; 1.
Toxin: Sodium channel inhibitor; Hydroxylation; Amidation;
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90249506; PubMed=2338142;
Hidaka Y., Sato K., Nakamura H., Kobayashi J., Ohizumi Y.,
Simonishi Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F6CB02ADB359813C CRC64;
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HYDROXYLATION.
HYDROXYLATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                  J. Biol. Chem. 260:9280-9288(1985).
[2]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR008036; Mu-conotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2568 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 264:29-32(1990).
                                                                                                                                                                                                       muscle sodium channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1TCG; 31-JAN-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-94.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A01786; MXKN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
22
13
19
22 AA;
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STRUCTURE BY NMR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 geographus.
                                             NCBI TaxID=6491;
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Matches
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PDB;
PDB;
  SOLUTION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE ST
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-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                          Score 25.5; DB 1; Length 22;
Pred. No. 5.9e+02;
2; Mismatches 1; Indel8
                                                                                     PDB; 1GIB; 08-NOV-96.
InterPro; LPRO00836; Mu-conotoxin.
PFEm; PF05574; Mu-conotoxin; 1.
Toxin; Sodium channel inhibitor; Hydroxylation; Amidation;
                                                                                                                                                                                                                                                                                            F50402BA93199E01 CRC64;
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HYDROXYLATION.
HYDROXYLATION.
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PHLC_STAIN
ID _FHLC_STAIN
AA PROP34;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                             AMIDATION.
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7
17
22
2599 MW;
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                                                                                                                                                                                                                                                                                                                                                 45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                 15 KCE---CRPKK 22
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PDB; 1GIB; 08-NOV-9
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Conservative 15 KC---ECRPKK 22

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muscle sodium channels.";
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                                                                                                                                                                                                                                                                                                                                                                                                                            15 KCE---CRPKK 22
                                                                                                                                                                                                                                                                                       Sodium channel
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                                                  Mu-conotoxin GIIIC.
                                                                                                                                                                                                                                                PIR; C23579; MXKN3
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  22 AA;
                                                                                                 NCBI TaxID=6491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steinman R.R.;
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DFTS_RAT
ID DFTS RAT
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MOD_RES
MOD_RES
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MOD_RES
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                                                                                                                                   Staphylococcus intermedius.",
Arch Bacchem Bloghys 335:102-108(1998).
-!- FUNCTION: REQUIRED. WITH SPHINGOMYELINASE TO EFFECT TRAGET CELL.
INSIS (HEMOLYSIS). THE PH OPTINUM IS 6.0-7.5. IT HAS A HIGH
SPECIFICITY FOR SPHINGOMYELIN, HYDROLYZES IXSOPHOSPHATIDYLCHOLINE
AT A MUCH LOWER RATE, BUT HAS NO ACTIVITY TOWARDS
PHOSPHATIDYLCHOLINE, PHOSPHATIDYLETHANOLAMINE, OR
PHOSPHATIDYLSERINE.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)0 = N-acylephingosine +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spinacia oleracea (Spinach).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, edicotyledons, core eudicots, (Caryophylales, Amaranthaceae, Spinacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kieselbach T., Pettersson U., Bystedt M., Schroeder W.P.;
Submitted (UDL-2000) to Swiss-Prot.
-1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
Chloroplast; Thylakoid.
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                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the neutral sphingomyelinase family. Hemolysis; Hydrolase; Toxin; Magnesium.
                                                                                                                           "Comparison of the beta-toxins from Staphylococcus aureus and
                                                                                                                                                                                                                                                                                               ; DB 1; Lengu..
5. 6.1e+02;
6; Indels
                                                                                    STRAIN=94-072594;
MEDLINE-97072006; PubMed=8914839;
Dziewanowska K., Edwards V.M., Deringer J.R., Bohach G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 1; Length 20;
Pred. No. 6.5e+02;
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Thylakoid lumenal 14.7 kDa protein (P14.7) (Fragment).
                                                                                                                                                                                                                                                                                    19 AA; 2089 MW; A50753FCF500F80E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984B7E4C52F5E3E0 CRC64;
                                                                                                                                                                                                                                                                                                       Score 25; DB 1
Pred. No. 6.1e+
3; Mismatches
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50.0%;
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30.8%;
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                                                                                                                                                                                                                                                                                                                                                                3 GENOAELKLATHN 15
                                                                                                                                                                                                                                                                                                                           4; Conservative
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                                                                                                                                                                                                                                    -!- COFACTOR: Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                            choline phosphate.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                 Local Similarity
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ID _CXM3_CONGE
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Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 260.9280-9288(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS. MU-TYPE
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                                                                                                                                      Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
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stimulating peptide from rat parotid glands.";
Chem. Pharm. Bull. 34:3803-3811(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-ARK-1988 (Rel. 07, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-MAR-1989 (Rel. 10, Last annotation update)
Dentinal fluid transport-stimulating peptide (DFT-stimulating peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 inhibitor; Hydroxylation; Amidation.
15 BY SIMILARITY.
20 BY SIMILARITY.
21 BY SIMILARITY.
6 HYDROXYLATION.
7 HYDROXYLATION.
17 HYDROXYLATION.
22 AMIDATION.
                                                                                                                                                                                                                                                                                                             MEDLINE=85261316; PubMed=2410412;
Cruz L.J., Gray W.R., Ollvera B.M., Zeikus R.D., Kerr L.,
Yoshikami D., Moczylowski E.,
"Conus geographus toxins that discriminate between neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24.5; DB 1; Length 22; Pred. No. 8.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F50402BA92A9813C CRC64;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            channel (VSSC).
SUBCRLLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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InterPro; IPR008036; Mu-conotoxin.
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MEDLINE=67131708; PubMed=5297832;
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                                                                                                              Conus geographus (Geography cone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF05374; Mu-conotoxin;
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45.5%;
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20-MAR-1987
20-MAR-1987
28-FEB-2003
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GON1_PETWA
ID GON1_PETWA
AC P04378;
DT 20-MAR-1987
DT 20-MAR-1987
DT 28-FEB-2003
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"The movement of acriflavine hydrochloride through molars of rats on a cariogenic and non-cariogenic diet."; J. South. Calif. Dent. Assoc. 35:151-157(1967).
-!- FUNCTION: This peptide stimulates the transport of dentinal fluid, which is important for the prevention of dental caries.
PIR; JJ0001; DIRT.
                                                                                                                        Gарв
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28-FRB-2003 (Rel. 41, Last annotation update)
Polistes mastoparan.
Polistes jadwigae (Paper wasp).
Rukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endoprerygeta; Hymenoptera; Apocrita; Aculeata; Vespoidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                         ·.
                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
215-MAR-2004 (Rel. 43, Last annotation update)
Textile convollant peptide.
Comus textile (Cloth-of-gold cone).
BLKATYOGA; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Neogastropoda; Conidea; Conidae; Conue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
Έ
                                                                                                                                                                                                                                                                                                                                                                 Cruz L.C., Ramilo C.A., Corpuz G.P., Olivera B.M.;
"Comus peptides: phylogenetic range of biological activity.";
Biol. Bull. 183:155-164(1992).
-!- FUNCTION: Causes convulsions mice.
-!- SUBCELLUIAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 23.5; DB 1; Length 23; Pred. No. 1.3e+03;
                                                                                                 Score 24; DB 1; Length 20;
Pred. No. 9.4e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: Expressed by the venom duct.
-!- SIMILARITY: Belongs to the conotoxin O-superfamily.
PIR; A59048; A59048.
                                                                  Dental caries, Parotid gland; Hormone.
SEQUENCE 20 AA; 2165 MW; FA164F2B6AF80D5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
AE99BDBB7DC8AD56 CRC64;
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                                                                                                                                                                                                                         23 AA.
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PROBABLE.
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21-JUL-1986 (Rel. 01, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.7%;
62.5%;
                                                                                                  18.0%;
80.0%;
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                                                                                                           Best_Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                              11 LQHNK 15
                                                                                                                                                                   7 LOHNE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toxin; Amidation.
DISULFID 2
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P01517;
                                                                                                                                                                                                                         CONTE
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DISULFID
MOD RES
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Matches
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WEDLINE-99449602; PubMed=10518793;

Gong N.L., Armugam A., Jeyaseelan K.;

Rostsynaptic short-chain neurotoxing from Pseudonaja textilis: cDNA
TPOSTSYNAPTES on and protein characterization.";

Eur. J. Biochem. 265:982-989(1999).

-! FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
acetylcholine receptors (nACR).

-! FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
c:- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
c:- FUNCTION: Lethal neurotoxin, becreted.

-! TISSUE SPECIFORITY: Mac6454; METMO-PELetcrospray.

-! ANS PRETROMETRY: Mac6454; METMO-PELetcrospray.

-! SIMILARITY: Belongs to the snake toxin family.

InterPro; IRRO03571; Stake toxin.

R PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.

TOXIN; Meurotoxin; Postsynaptic neurotoxin;

MACHALLAND R PROSITE; POSTESPANDELIC neurotoxin;

MACHALLAND R PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE; PROSITE
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niral Y., Ueno Y., Yasuhara T., Yoshida H., Nakajima T.;
"A new mast cell degranulating peptide, polistes mastoparan, in the venom of Polistes jadwigae.";
Biomed. Res. 1.185-187(1980).
-!- FUNCTION: Mast cell degranulating peptide. Activates G proteins that couple to phospholipase C.
PIR, AD1780, OWMAPP.
Mast cell degranulation, Amidation.
MOD_RES.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotaxin) update)
Short neurotoxin N2 (Alpha neurotoxin) (Fragment).
Pseudonaja textilis (Bastern brown make).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleogtomi; Lepidae, Acanthophiinae; Scleroglossa; Serpentes; Colubroidea; NCBI_TaxID=8673;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.3%; Score 23; DB 1; Length 14; 100.0%; Pred. No. 9.4e+02; tive 0; Mismatches 0; Indels
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SEQUENCE 14 AA; 1636 MW; 26472A53BF4778D8 CRC64;
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Pred. No. 1e+03;
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(Rel. 04, Last sequence update)
(Rel. 41, Last annotation update)
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Best Local Similarity
Matches 3; Conserv
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4 GQHV 7
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                                                                                                                                                J. Biol. Chem. 261:4812-4819(1986).
-!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating
                                                                                                                  Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J., "Primary structure of gonadotropin-releasing hormone from lamprey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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-!- MISCELLANBOUS: On the 2D-gel the determined pI of this unknown protein is: 6.93, its MW is: 81.6 kDa.
Aarhus/Ghent-2DPAGE; 1617; IEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Unknown protein from 2D-page of epidermal keratinocytes (Spot 1617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
           (Inliberin I).
Butercomyzon marinus (Sea lamprey).
Buterryezon marinus (Sea lamprey).
Buterryezon: Metacoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Petromyzon.
NCBI_TaxID=7757;
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                                                                                                                                                                                                                                     InterPro; irrovever.

Pfam; PF00446; GnRH; 1.

PROSITE; PS00473; GNRH; 1.

Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

1 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Keratinocytes;
MEDLINE-93162043; PubMed=1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Sonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
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75.0%; Pred. No. 1.2e+03;
"".emarches 0; Indels
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1E4B36237B1735AB CRC64;
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Pred. No. 9.6e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 AA.
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-:- STHARATY: Belongs to the GRRH family.
PTR, A01412; RHLMGS.
InterPro; IPR002012; GRRH.
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Best Local Similarity
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                                                                                          TISSUE-Brain;
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Marina A., Wollberg Z., Fideninger G.;

Marina A., Wollberg Z., Fideninger G.;

Marina A., Wollberg Z., Fideninger G.;

Marina A., Wollberg Z., Fideninger G.;

Marina M., Wollberg Z., Fideninger G.;

Marina M., Wollberg Z., Fideninger G.;

Marina M., Wollberg J., Marina M., Mari
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Toxin Tcl (Alpha-KTx 13.1).
Tityus cambridgei (Amazonian scorpion).
Ekwaryots, Merazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Tityus.
                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Atractaspididae; Atractaspis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 486:117-120(2000).
-1- FUNCTION: Blocks reversibly Shaker B potassium channels. Also
displaces binding of noxiustoxin to mouse brain synaptosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                           Atractaspis engaddensis (Israeli burrowing asp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.1e+03;
                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
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PRT;
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MEDLINE=90033283; PubMed=2509240;
                                                                                                                                                                                                                                                                                    Sarafotoxin-D (S6D) (SRTX-D)
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STANDARD;
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         -!- SUBCELLUIAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- MASS SPECTAMETRY: MW-246.4; METHOD-MALDI.
-!- MANIZARITY: Belongs to the short scorpion toxin family. Potassium channel inhibitor subfamily.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:001970; F:potassium channel inhibitor activity; IDA.
GO; GO:001970; F:corn activity; IDA.
GO; GO:001970; F:corn activity; IDA.
FOOTE: PROSITE: PSOIL138; SCORP.SORP.TOXIN; PALSE NEG.
TOXIN; Neurotoxin; Ionic channel inhibitor.
Potassium channel inhibitor.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
Electrophoridae; Electrophorus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conti-Tronconi B.M., Hunkapiller M.W., Lindstrom J.M., Raftery M.A., "Subunit structure of the acetylcholine receptor from Electrophorus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 79:6489-6493 (1982).
-!- FUNCTION: After binding acetylcholine, the AChR responds by an extensive change in conformation that affects all subunits and leads to opening of an ion-conducting channel across the plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Pentamer of two alpha chains, and one each of the beta, delta, and gamma chains.
                                                                                                                                                                                                                                               INTERACTION WITH CA(2+)-ACTIVATED K(+)
CHANNELS (POTENTIAL).
D59BFADEC9F31700 CRC64;
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                                                                                                                                                                                                                                                                                                              Score 22; DB 1; Length 23;
Pred. No. 2.3e+03;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
02-MAR-1989 (Rel. 11, Last annotation update)
Acetyl-Choline receptor protein, gamma chain (Fragment).
Electrophorus electricus (Electric eel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 AA; 2717 MW; DA88F7E9900C024B CRC64;
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Similarity 33.3%;
2; Conservative
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Search completed: March 8, 2004, 11:46:49 Job time : 12 secs

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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		EI .	095376	025134	QSTGW6	Q99LQ2	025086	012066	Q85WB3	Q85WB1	Q85WA9	Q86MIN6	Q86MN2	QBGMMO	QBSKYO	063058	Q9RBV0	097668
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5.5 3.3 3.3 3.3 3.3 5.0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 8 ft 3 34 day by no. 1666 By	PRELIMINARY;
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H H H H G G G G G G G G G G G G G G G G	25.376	RESULT Q25134 ID Q2 AC Q3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMED, U09939; AAA18629.1; -. GO; GO:0005634; C:nucleus; IEA. GO; GO:0005634; C:nucleus; IEA. GO; GO:0003500; F:transcription factor activity; IEA. GO; GO:000355; P:realization of transcription, DNA-dependent; IEA. InterPro; IPR001356; Homeobox. Pfam; PF00046; homeobox; 1. DNA-binding; Homeobox; Nuclear protein.
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kennett C.V.D.; "Cloning and Sequencing of Homeoboxes from the Ascidian Herdmania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                          21.8%; Score 29; DB 11; Length 23; 43.8%; Pred, No. 9.4e+02; arive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.1%; Score 28; DB 5; Length 21; 44.4%; Pred. No. 1.3e+03; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
BMBL; BC0022776, AAH02276.1; -.
Hypotherical protein.
SEQUENCE 23 AA; 2223 MW; 2A4C872213B58B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herdmania momus (Brown sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Herdmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AA; 2650 MW; AB7FF3AF1FA659C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2003 (TrEMBLrel. 24, Last annotation update)
Clone AHOX4 homeobox protein (Fragment).
                                    Q99DQ2 PRELIMINARY; PRT; 23 AA.
Q99DQ2 Q99DQ2;
Q1-UUN-2001 (TEMBLrel. 17, Created)
O1-UUN-2001 (TEMBLrel. 17, Last sequence update)
O1-OCT-2003 (TEMBLrel. 25, Last annotation update)
Hypotherical protein.
Ms musculus (Mouse).
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01-JUL-1997 (TrEMBLrel. 04, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GQHIGEMSFLQHNKCE 17
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Best Local Similarity 43.00,
A Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Conservative
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1 NRYLCRPRR 9
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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012066
ID 01206
AC 01206
DT 01-JU
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                                                                                                                                                                                                                                                                                                XX MEDLINE—9372986; PubMed=7689904;
XM MEDLINE—9372986; PubMed=7689904;
Degnan B.M., Morse D.E.;
Degnan B.M., Morse D.E.;
Identification of eight homeobox-containing transcripts expressed during larval development and at metamorphosis in the gastropod during larval development and at metamorphosis in the gastropod during larval development and at metamorphosis in the gastropod during larval development and at metamorphosis in the gastropod during larval development and at metamorphosis in the gastropod RM BL, X79372; CAA55917.1; -.

RM BL, X79372; CAA55917.1; -.

RM GO; GO:0005634; C:nucleus; IEA.

RG; GO:0003700; F:transcription factor activity; IEA.

RG; GO:000355; Homeobox.

REPLANCE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPAGE OF CAMPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Onygenalus, Arthrodermataceae, mitosporic Arthrodermataceae,
Microsporum.
NCBI_TaxID=82078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Uthman A., Dockal M., Ban J., Rezaie S., Soeltz-Szoets J.,
Tschachler E.;
                                                                                                 Haliotis rufescens (California red abalone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
NCBI_TaxID=6454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 30; DB 3; Length 23; 80.0%; Pred. No. 6.3e+02; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31; DB 5; Length 23; Pred. No. 4.2e+02; i. Mismatches 2; Indels
                                                                                                                                                                                                                                              Degnan B.M.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON TER 1 1 1 1 1 1 2 23 23 SEQUENCE 23 AA; 2793 MW; CC387AE7BDA6C44D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-CTT-2002 (TrEMBLrel. 22, Last annotation update)
Metallothionein.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 AA.
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Best Local Similarity 55.6%;
Matches 5; Conservative
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                                                                 Hrox3 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKYLCRPRR 10
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Matches
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Q8TGW6
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Sugita M.;
"The intergenic region between rps11 and petD of the moss chloroplast
DVA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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    Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Bryidae; Hypnales; Plagiotheciaceae; Plagiothecium.
NCBI_TaxID=90297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Bryophyta,
Bryopsida, Bryidae, Bryales, Bartramiaceae, Bartramia
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
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GO; GO:0009567; C:chloroplast; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
Chloroplast; Ribosomal protein.
NON_TER 1 1 1
SEQUENCE 22 AA; 2638 MW; 130D2ADC3C3D2C04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBJ, AB098726, BAC64961.1, -.
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.1%; Score 28; DB 8; Length 22; Best Local Similarity 33.3%; Pred. No. 1.3e+03; Matches 6; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.1%; Score 28; DB 8; Length 22; 33.3%; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                 Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosomal protein S11 (Fragment).
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast; Ribosomal protein.

NON TER 1 1 1 SEQUENCE 22 AA; 2638 MW; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VRDVTPMPHN--GCRPPK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 IGEMSFLOHNKCECRPKK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IGEMSFLQHNKCECRPKK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 VRDVTPMPHN--GCRPPK 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Sugita M.;
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=52976;
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Q85WA9
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                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-97296261; PubMed=9151845;

Turelli P., Guiquen F., Mornex J.F., Vigne R., Querat G.;

Turelli P., Guiquen R., Mornex J.F., Vigne R., Querat G.;

"dUTPase-minus caprine arthritis-encephalitis virus is attenuated for pathogenesis and accumulates G-to-A substitutions.";

J. Virol. 71:4522-4530(1997).

EMBE, U81420; AAC57935.1; -.

NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugita M.;
"The intergenic region between rps11 and petD of the moss chloroplast
DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Bryidae; Hypnales; Hylocomiaceae; Hylocomium.
NCBL_TaxID=53007;
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                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%; Score 28; DB 15; Length 21; 36.4%; Pred. No. 1.3e+03; tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; ABO98724; BAC64957.1; -. GO; GO:0009507; C:chloroplast; IEA. GO; GO:0009507; C:chloroplast; IEA. GO; GO:0003735; F:structural constituent of ribosome; IEA. Chloroplast; Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.1%; Score 28; DB 8; Length 22; 33.3%; Pred. No. 1.3e+03; ive 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                    21 AA; 2497 MW; A377E24541CCEFA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 AA; 2638 MW; 130D2ADC3C3D2C04 CRC64;
01-JUL-1997 (TrEMBLrel. 04, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-UN-2003 (TrEMBLrel. 24, Created)
01-UN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosomal protein S11 (Fragment).
                                                                                                                 Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11660;
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                                                                                           Caprine arthritis encephalitis virus (CAEV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hylocomium splendens (Mountain fern moss).
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                                             Envelope glycoprotein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 OHNKCECRPKK 22
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5 ESNKWTCAPRR 15
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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"Sequence analysis and coding potential of the holoparasitic flowering plant genus Cuscuta.";
Thesis (2002), popartment of Institute of Botany.
Thesis (2002), copartment of Institute of Botany.
EMBL; A.4439611; CAD28796.1; -.
EMBL; A.4439611; CAD28796.1; -.
EMBL; A.4439611; CAD28796.1; -.
GO; GO:0005840; C:chloroplast; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPRO61971; Ribosomal S11.
Pfam; PF00411; Ribosomal S11; I.
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Bukaryora; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamida; Solamales; Convolvulaceae; Cuscuta.
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                                                                                                                                                             Bukaryota, Metazoa, Mollusca, Bivalvia, Protobranchia, Nuculoida,
Nuculanoidea, Sareptidae, Yoldia.
NCBL_TaxID=177101;
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Pred. No. 1.6e+03;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 28; DB 5; Length 23;
Pred. No. 1.4e+03;
3; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 AA; 2864 MW; 0F387FF3AF1FD45F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cuscuta reflexa (Southern Asian dodder).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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Best Local Similarity 44.4%,
-%aq 4; Conservative
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5 MPHN--GCRPPK 14
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     HOX3.
Yoldia eightei
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Barucca M., Olmo E., Canapa A.;
"Hox and ParaHox genes in bivalve molluscs.";
"Hox and ParaHox genes in bivalve molluscs.";
submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ53452; CAD58901.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001356; Homeobox.
Homeobox; DNA-binding; Nuclear protein.
                                                                                                            Barucca M., Olmo E., Canapa A.;
"Hox and ParaHox genes in bivalve molluscs.";
submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AJ534448; CAD58897.1; -.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
ProDom; PD000010; Homeobox; 1.
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Mytiloidea; Mytilidae; Mytilus.
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Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; DB 5; Length 23;
Pred. No. 1.4e+03;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 AA; 2864 MW; 0F387FF3AF1FD45F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01.-UN-2003 (TrEMBLrel. 24, Created)
01.-UN-2003 (TrEMBLrel. 24, Last sequence update)
01.-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
HOX3 homeodomain protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                       Homeobox; DNA-binding; Nuclear protein.
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Solenoidea; Pharidae; Ensis.
NCBI_TaxID=120427;
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Matches 4; Conserv
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Q86MN2
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Chloroplast.
Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Lamiales; Orobanchaceae; Orobanchaceae incertae sedis;
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STRAIN=R9; TRANSPOSON=Tn1404;
MEDLINE=20011227; PubMed=10543801;
Schnabel E.L., Jones A.L.;
"Distribution of terracycline resistance genes and transposons among phylloplane bacteria in Michigan apple orchards.";
Appl. Environ. Microbiol. 65:4898-4907 (1999).
NON_TER 11 11
                                                                                                                                                                                                                                                                                    Lusson N., Delavault P., Thalouarn P., "The rock gene from Lathraea (holoparasitic) is not transcribed by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales, Pseudomonadaceae, Pseudomonas.
NSE TaxID=101164;
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                                                                                                                                                                                                                                                                                                                  plastid-encoded RNA polymerase.";

L Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

EMBL, AF030993; AAC16521.1;

C GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005640; C:ribosome; IEA.

GO; GO:0005840; C:ribosome; IEA.

GO; GO:0005841; E:ribosome; IEA.

R GO; GO:0005412; P:protein biosynthesis; IEA.

R GO; GO:0006412; P:protein biosynthesis; IEA.

R ThterProt IPR001971; Ribosomal S11.

R Fam; PF00411; Ribosomal S11; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h Similarity 50.0%; Pred. No. 1.7e+03, 6; Conservative 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER 1 1 1
SEQUENCE 19 AA; 2245 MW; 130D2AB3FE680B24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AA; 1307 MW; D00B18E258704416 CRC64;
                                            01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Ribosomal protein S11 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Resolvase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                19 AA.
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                PRT;
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              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LQHNKCECRPKK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=41911;
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Q9RBV0
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Search completed: March 8, 2004, 11:47:40 Job time : 39 secs

16.

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March 8, 2004, 11:13:12; Search time 52 Seconds (without alignments) 124.973 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                       1586107 seqs, 282547505 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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1 QGQHIGEMSFLQHNKCECRPKKD
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Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003bs:* A_Geneseq_29Jan04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Aau04523 Human VEG	Aau08454 Peptide A	Aab10862 ScVEGF2 c	Aabl0860 ScVEGF2 c	Aaw23802 VEGF/VPF	Aaw53383 Tumour me	Aaw53444 Vascular	Aaw74627 Amino aci	Amino	Aaw55950 Human vas	Aaw55949 Human vas	Aaw97382 A VEGF/VP	Aay57613 Human VEG	Aay57674 Human vas		•		Aab74567 VEGF VPF	Aab74575 VEGF VPF	Aab97893 Human VEG	Aab97894 Human VEG	Aaw53443 Vascular	Aaw74687 Amino aci	Aaw55948 Human vas	Aay57673 Human vas
SUMMARIES		AAU04523	AAU08454	AAB10862	AAB10860	AAW23802	AAW53383	AAW53444	AAW74627	AAW74688	AAW55950	AAW55949	AAW97382	AAY57613	AAY57674	AAY59616	AAY58055	AAB74566	AAB74567	AAB74575	AAB97893	AAB97894	AAW53443	AAW74687	AAW55948	AAY57673
Length DB		23 4	13 4	21 3		12 2					12 2			12 3	12 3	12 3	12 3	12 4	12 4	12 4	12 4	12 4	12 2	12 2	12 2	12 3
* Query Match Le		100.0	59.4	56.4	56.4	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9	53.4	53.4	53.4	53.4
Score		133	79	75	75	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	73	71	71	71	71
Result No.	1 1 1	-	7	m	4	2	٥	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aay59615 Vascular Aab74565 VEGF VPF AAb57892 Human VEG Aw51445 Vascular		Aay59617 Vaecular Aab74568 VEGF VPF Aab97895 Human VEG	Aaw53442 Vascular Aaw74686 Amino aci Aaw55947 Human vas	Aay57672 Human vas Aay59614 Vascular Aab74564 VEGF VPF	Aab97891 Human VEG Aaw53441 Vascular Aaw74685 Amino aci Aaw55946 Human vas
3 AAY59615 4 AAB74565 4 AAB97892 2 AAW53445	2 AAW74689 2 AAW55951 3 AAY57675	3 AAY59617 4 AAB74568 4 AAB97895	2 AAW53442 2 AAW74686 2 AAW55947	3 AAYS7672 3 AAYS9614 4 AAB74564	4 AAB97891 2 AAW53441 2 AAW74685 2 AAW55946
2222	1222	1221	12 12 13	222	12 12 12 12 12 12 12 12 12 12 12 12 12 1
71 53.4 71 53.4 71 53.4 70 52.6		70 52.6 70 52.6 70 52.6		വവവ	67 50.4 66 49.6 66 49.6 66 49.6
22 23 23 24	333	3 3 3 5 4 5 5	36 37 38	39 41 11	4 4 4 4 2 6 4 6

ALIGNMENTS

E TINGG	
AAII04523	523
a a a	AAU04523 standard; peptide; 23 AA.
	AAU04523;
×	
	26-SEP-2001 (first entry)
ž	
DE	Human VEGF amino acids Gln113-Asp135.
¥2	Human: VEGF: vascular endothelial growth factor: angiogenesis:
	diabetic retinopathy; chronic inflammation.
	Homo sapiens.
	WO200152875-A1,
X	
	26-JUL-2001.
×	
	18-JAN-2001; 2001WO-US001533.
	18-JAN-2000; 2000US-0176293P,
	16-MAY-2000; 2000US-0204590P.
	(LUDW-) LUDWIG INST CANCER RES.
×	
	Achen MG, Hughes RA, Stacker S, Cendron A;
9	WDI: 3001-443349/47

Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine WPI; 2001-442248/47.

Example 1; Page 91; 102pp; English. from an er

The sequence represents Human VEGP (vascular endothelial growth factor) amino acids Gln113-Asp1353, used to replace the C-terminal 23 residues of VEGP-D to make a hybrid theoretical molecule for 3 dimensional modelling. The sequence is used in a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a peptide loop fragment from an exposed loop of a growth factor protein and cyclising the peptide by oxidising the cysteine residues. The monocyclic peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic peptides) and a cyclic peptide with at least one

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amino acid deleted prior to cyclisation are used to interfere with an angiogenesis, neovascularisation or lymphangiogenesis in a mammal with a condition characterised by angiogenesis, neovascularisation or condition characterised by angiogenesis, neovascularisation or lymphangiogenesis. The condition is diabetic retinopathy, psoriasis, arthropathy, hemangioma, vascularised malignant or benign tumnour, post-recovery cerebrovascular accident, post-angioplasty restenosis, head, heat or cold trauma, substance-induced neovascularisation of the liver, excessive hormone-related angiogenic dysfunction, diabetes induced neovascular sequelae, hypertension induced neovascular sequelae, corresponded in induced neovascular sequelae, corresponded in induced neovascular sequelae, corresponded in induced neovascular sequelae, propried in a condition characterised by permeability in a mammal (the mammal has a condition characterised by pleura, or brain. The peptides are used to image blood vessels and lymphatic vasculature. The monomeric and bicyclic peptides are used to interfere with at least one biological activity induced by VBGF, VBGF-C or -D and are also used in combination with an anti-inflammatory agent, to treat a chronic inflammation, especially rheumatoid arthritis, psoriasis and diabetic retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 23 AA;
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/ Match 100.0%; Score 133; DB 4; Length 23; Local Similarity 100.0%; Pred. No. 1.1e-13; tes 23; Conservative 0; Mismatches 0; Indels 1 QGQHIGEMSFLQHNKCECRPKKD 23 1 QGQHIGEMSFLQHNKCECRPKKD 23 Query Match Best Loc Matches ð 셤

Peptide A9 encoded by human VEGF-A forward primer A9-F. AAU08454 standard; peptide; 13 AA. (first entry) primer; mutant; mutein. 21-NOV-2001 AAU08454; RESULT 2

Human, vascular endothelial growth factor, VEGF-A, vasculogenesis, angiogenesis, blood vessel, cancer, proliferative retinopathy, psoriasis, age-related macular degeneration; rheumatoid arthritis, cardiovascular;

WO200162942-A2. Homo sapiens. Synthetic.

26-FEB-2001; 2001WO-US006113. 30-AUG-2001.

(LUDW-) LUDWIG INST CANCER RES (LICN) LICENTIA OY. 25-FEB-2000; 2000US-0185205P. 18-MAY-2000; 2000US-0205331P.

Ë WPI; 2001-536640/59. Jeltsch Alitalo K,

Polypeptides that bind cellular receptors for vascular endothelial growth factors, polynucleotides encoding them. N-PSDB; AAS12810

Claim 9; Fig 7D; 261pp; English.

The present invention relates to polypeptides that bind cellular receptors for vascular endothelial growth factors (VEGFs), the polynucleotides encoding them, and their use for identifying agents that

modulate interactions between VEGFs and their receptors. VEGFs and their receptors play an important role in vasculogenesis, the development of the embryonic vasculature from early differentiating endothelial cells and angiogenesis, the process of forming new blood vessels from preexisting ones. Modulators of interactions between VEGF and its receptors may be used to treat dysfunction of the endothelial cell regulatory proliferative retinopathies, age-related macular degeneration, rheumatoid arthritis and psoriasis. The polypeptides of the invention exhibit unique receptor binding profiles compared to known naturally occurring VEGFs. AMU08446-AAU08446-AAU08446-AAU08446-AAU08446-AAU08446-AAU08446-AAU08 Score 79; DB 4; Length 13; 59.4%; Sequence 13 AA; Query Match

ö Gaps ; 1.9e-05; les 0; Indels 100.0%; Pred. No. 1.9 ive 0; Mismatches AAB10862 standard; protein; 21 AA. (first entry) 11 LQHNKCECRPKKD 23 1 LOHNKCECRPKKD 13 Best Local Similarity 100. Matches 13; Conservative 02-FEB-2001 AAB10862; RESULT 3 AAB10862 à 셤

ö

Gaps . 0 ScVEGF2 construct protein fragment SEQ ID NO: 34.

nervous system; inner organ; hematopoietic system; immune system; joint; support tissue; immunization. MVP; multivalent protein; treatment; dressing; skin; mucus; musculature;

26-FEB-2000; 2000WO-EP001612. WO200053790-A1. Homo sapiens. 14-SEP-2000.

Synthetic.

(AVET) AVENTIS PHARMA DEUT GMBH. 10-MAR-1999;

Nettelbeck D, Sedlacek H, Mueller R; 2000-572272/53. Kontermann R,

Cell specific multivalent proteins useful for targeting specific cells N-PSDB; AAA98171.

Example 2; Page 63-64; 81pp; German.

for the treatment of disease

This invention describes a method for the production of a novel cell specific multivalent protein (MVP). The invention also describes (1) a nucleic acid construct, which encodes an MVP; (2) a bacterium, yeast or mucheler caid construct of (1) is introduced; (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP comprising a scFV with a binding site for the adenoviral fibre protein or COD3 molecule and two VEBF units, bound by a peptide linker; and (6) a complex comprising at least two MVPS as above (in which each single ligand can be 0=1). The MVP, optionally bound to a vector, is useful for production of a remedy to treat cells outside tissue by dressings for production of a remedy to treat cells outside tissue by dressings for skin, mucus, nervous systems, inner organs, hematopoletic systems, immune systems, musculature, support tissues or joints and to immunize to

Query Match

SXS

Local

Best Loca Matches

g 8

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Human vascular endothelial cell growth factor-vascular permeability factor antigen - and monoclonal antibody against it, useful for diagnosis and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A total of 67 overlapping peptides, each of 12 amino acids in length, were synthesised to cover the 121 amino acid sequence of human vascular endothelial cell growth factor/vascular permeability factor (VBGF/VPF). Five of the peptides reacted with an anti-VPF monoclonal antibody. Three of these antigenic peptides all included the sequence Lys-Pro-Ser-Cys-Val-Pro-Leu-Met-Arg (AAW23801). The other two 12mers had the sequences Ser-Phe-ieu-Gln-His-Asn-Lys-Cys-Glu-Cys-Arg-Pro (AAW23802) and Lys-Cys-Glu-Cys-Arg-Pro (AAW23802) and Lys-Cys-Glu-Cys-Arg-Pro-Lys-Lys-Arg-Arg-Ala-Arg (AAW23803). The antigenic peptides diseases such as cancer
                                                                                                                                                                                                                                           Vascular endothelial cell growth factor; VEGF; VPF; antigen; vascular permeability factor; anti-VEGF; monoclonal antibody; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour metastasis inhibitor; human; VEGF; metastasis therapy; vascular endothelial cell growth factor; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 73; DB 2; Length 12;
100.0%; Pred. No. 0.00015;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                       VEGF/VPF antigen sequence SFLOHNKCECRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour metastasis inhibitor peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW53383 standard; peptide; 12 AA.
                                                                                 AAW23802 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 6; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TOAG ) TOA GOSEI CHEM IND LTD.
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                                                                                                                                                                (first entry)
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SFLQHNKCECRP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12 AA;
                                                                                                                                                                                                                                                                                                                                                  JP09124697-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995;
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Homo sapiens.
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                12-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1997.
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                                                                                                                        AAW23802;
                                          RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes a method for the production of a novel cell specific multivalent protein (MVP). The invention also describes (1) a nucleic acid construct, which encodes an MVP; (2) a bacterium, yeast or (3) the MVP bound to a vector; (4) production of an MVP; (5) an MVP comprising a scFV with a binding site for the adenoviral fibre protein or CD3 molecule and two VEBF units, bound by a peptide linker; and (6) a complex comprising at least two MVPS as above (in which each single ligand can be 0=1). The MVP, optionally bound to a vector, is useful for production of a remedy to treat cells outside tissue by desssings for skin, mucus, nervous systems, inner organs, hematopoietic systems, immune systems musculature, support tissues or joints and to immunize to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVP; multivalent protein; treatment; dressing; skin; mucus; musculature; nervous system; inner organ; hematopoietic system; immune system; joint; support tissue; immunization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specific multivalent proteins useful for targeting specific cells
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                                                                               56.4%; Score 75; DB 3; Length 21; 100.0%; Pred. No. 0.00013; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kontermann R, Nettelbeck D, Sedlacek H, Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                  ScVEGF2 construct protein fragment SEQ ID NO: 29.
                                                                                                                                                                                                                                                                                                       AAB10860 standard; protein; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AVET ) AVENTIS PHARMA DEUT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 58; 81pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for the treatment of disease.
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prevent or treat diseases
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                                                                                                                     Conservative
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nes 12; Conserv
                                                                                                  Similarity
12; Conserv
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N-PSDB; AAA98168.
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                                        Sequence 21 AA;
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Cell

Synthetic.

AAB10860;

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Gaps ;

Query Match

Best Loca Matches

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peptide from the present invention. The present invention describes a tumour metastasis inhibitor consisting of vascular endothelial cell growth factor (VEGF) inhibitor. In an example, anti-vascular endothelial cell growth factor polyclonal antibody was produced, and an antibody was carried out. The hybridoma was selected and cultured. The monoclonal antibody was identified. A peptide corresponding to part of the monoclonal antibody was identified. A peptide corresponding to part of the amino acid sequence of vascular endothelial cell growth factor was prepared. A peptide reacting with the monoclonal antibody was identified. The amino acid sequence of vascular endothelial cell growth factor was prepared. A peptide reacting with the monoclonal antibody was identified. The monoclonal antibody was identified. The can be effectively applied in metastasis inhibitor. The drug can be effectively applied in metastasis
                     present sequence represents a vascular endothelial cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vascular endothelial growth factor; VEGF; vascular permeability factor; VPF; inhibition; malignant tumour; benign tumour; liver cirrhosis; inflammation of peritoneum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a vascular endothelial growth factor/vascular permeability factor (VEGF/VPF) peptide used in the method of the invention as an inhibitory agent. The inhibitory agent is used for the treatment of retention of body fluid during disease states, e.g. malignant and benign tumours, inflammation of peritoneum, ascites, and
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An inhibitory agent for the re-retention of body fluid - useful for treating this side-effect of associated disease states.
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Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 54.9%; Score 73; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of the VEGF/VPF peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW74627 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 2; 8pp; Japanese.
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  $$99999998888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a tumour metastasis inhibitor peptide from the present invention. The present invention describes a tumour metastasis inhibitor consisting of vascular endothelial cell growth factor (VEGF) inhibitor. In an example, anti-vascular endothelial cell growth factor polyclonal antibody was produced, and an antibody.

Droducing cell was prepared. A myeloma cell was prepared and cell fusion was carried out. The hybridoma was selected and cultured. The monoclonal antibody was collected and purified. The reaction site of the amino antibody was identified. A peptide corresponding to part of the amino cold sequence of vascular endothelial cell growth factor was prepared. A peptide reaction was into the amino peptide reacting with the monoclonal antibody was used as a tumour metastasis inhibitor. The drug can be effectively applied in metastasis therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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growth factor inhibitor,
                                                                                                                                                                                                                                                                          Tumour metastasis inhibitor - consists of vascular endothelial cell
growth factor inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.9%; Scur.
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW53444 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 2; 12pp; Japanese.
                                                                                                                                                                              (TOAG ) TOA GOSEI CHEM IND LID.
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                                                                                       97JP-00181769.
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                                                                                                                                                                                                                            WPI; 1998-267032/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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JP10087509-A
                                                                                       23-JUN-1997;
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                                           07-APR-1998
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Matches

RESULT 7

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9 SFLQHNKCECRP 20

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Homo sapiens JP10245347-A.

21-DEC-1998

AAW74688;

AAW74688

RESULT

28-FEB-1997; 28-FEB-1997;

14-SEP-1998

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The present sequence represents a peptide fragment from human vascular permeability factor (VPE), which is used in the example of the present invention to produce a monoclonal antibody against human VPE. The monoclonal antibody produced was designated MV 813. The monoclonal antibody was used in a novel carcinostatic of the present invention, comprising an anti-vascular endothelial growth factor (VEGF)/VPF antibody (Ab), and mitomycin or cisplatin. The carcinostatic improves the effect
                                                                                                                                                                                                         Carcinostatic comprises anti-vascular endothelial growth factor antibody - and mitomycin or cisplatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinostatic comprises anti-vascular endothelial growth factor antibody - and mitomycin or cisplatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a peptide fragment from human vascular permeability factor \{VPF\}, which is used in the example of the present invention to produce a monoclonal antibody against human VPF. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, vascular permeability factor; VPF; mitomycin; cisplatin; vascular endothelial growth factor; VEGF; carcinostatic; anti-tumour; monoclonal antibody; MAb; MV 833.
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t; Pred, No. 0.00015;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.9%; Scur-
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                                                            the known anti-tumour agents
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                                                                                                                                 (TOAG ) TOA GOSEI CHEM IND LID
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                                                              96JP-00143621
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 LOHNKCECRPKK 22
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                                                                                                                                                                     WPI; 1998-059107/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12 AA;
                                                              14-MAY-1996;
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Homo Bapiens.
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                                                                                                14-MAY-1996;
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                          25-NOV-1997
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                                                                                                                                                                                                                                                    Vascular endothelial growth factor; VBGF; vascular permeability factor; VPF; inhibition; malignant tumour; benign tumour; liver cirrhosis; inflammation of peritoneum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of a vascular endothelial growth factor/vascular permeability factor (VEGF/VPF) peptide used in the method of the invention as an inhibitory agent. The inhibitory agent is used for the treatment of retention of body fluid during disease states, e.g. malignant and benign tumours, inflammation of peritoneum, ascites, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, vascular permeability factor; VPP; mitomycin; cisplatin;
vascular endothelial growth factor; VEGF; carcinostatic; anti-tumour;
monoclonal antibody; MAb; MV 833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An inhibitory agent for the re-retention of body fluid - useful for treating this side-effect of associated disease states.
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; Pred. No. 0.00015;
0; Mismatches 0; Indels
                                                                                                                                                                                                                 Amino acid sequence of the VEGF/VPF peptide 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human vascular permeability factor peptide 61.
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100.0%; Pred. No. v..
                                                                                                         AAW74688 standard; peptide; 12 AA.
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SFLQHNKCECRP
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Best Local Similarity
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liver cirrhosis Sequence 12 AA;

12;

Matches

8 g Homo sapiens. JP09301888-A.

Synthetic.

AAW55950;

RESULT 10

AAW55950

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Gaps ; 0

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A thermotherapy method has been developed which involves destroying the tumour site by hot temperature and administering vascular endothelial cell growth factor (VBGP)/ vasopermeability factor (VPR) antagonist. The method is useful for the treatment of various cancers. The VBGR/VPF antagonist has cytostatic activity and is a tumourigenesis inhibitor. Proliferation of the tumour is suppressed effectively. AAY57612 to AAY57614 represent specifically claimed human VBGF/VPF peptides. AAX57615
                                                                                                                                                                                                                                                                                                                                                                Thermotherapy for treatment of various cancers - involves destroying the tumor site by hot temperature and inhibiting angiogenesis effect by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, vascular endothelial cell growth factor; VEGF; VPF; VEGF-121; vascopermeability factor; tumour; monoclonal antibody; thermotherapy; cancer; angiogenesis; cytostatic; tumourigenesis; inhibition; proliferation; suppression; antitumour.
                           Human, vascular endothelial cell growth factor; VEGF; VPF; VEGF-121; vasopermeability factor; tumour; monoclonal antibody; thermotherapy; cancer; angiogenesis; cytostatic; tumourigenesis; inhibition; proliferation; suppression; antitumour.
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Pred. No. 0.00015;
0; Mismatches 0; Indels
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100.0%; Pred. No. v...
... 0; Mismatches
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Human VEGF/VPF peptide SEQ ID NO:2.
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hes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              VEGF/VPF antagonist.
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                                                                                                                                                                JP11310537-A.
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                                                                                                                                                                                        ;
       monoclonal antibody produced was designated MV 833. The monoclonal antibody was used in a novel carcinostatic of the present invention, comprising an anti-vascular endothelial growth factor (VEGF)/VPF antibody (Ab), and mitomycin or cisplatin. The carcinostatic improves the effect of the known anti-tumour agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW97381-82 represent antagonist of vascular endothelial growth factor (VEGF)/vascular permeability factor (VPF). The peptides are used in an anticancer agent, which is used to inhibit growth of a tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antagonist; vascular endothelial growth factor; VEGF;
vascular permeability factor; VPF; anticancer agent; growth inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New anticancer agent - comprises VEGFF/VPF and bFGF antagonists.
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                                                                                                                                                       54.9%; Score 73; DB 2; Length 12; 100.0%; Pred. No. 0.00015; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A VEGF/VPF antagonist used in an anticancer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.9%; Score 73; DB 2; L6
100.0%; Pred. No. 0.00015;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                     AAW97382 standard; peptide; 12 AA.
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Matches 12; Conservative
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Query Match

23-FEB-1999.

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14-MAY-1999

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A thermotherapy method has been developed which involves destroying the tumour site by hot temperature and administering vascular endothelial cell growth factor (VPGF)/ vasopermeablility factor (VPGF) antagonist. The method is useful for the treatment of various cancers. The VEGF/VPF antagonist has cytostatic activity and is a tumourigenesis inhibitor. Proliferation of the tumour is suppressed effectively. AMS7615 to AANS7614 represent poscifically claimed human VEGF/VFF peptides. AMS7615 to AANS7619 represent human VEGF-121 peptides used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is a fragment of human vascular endothelial cell growth factor (VBGF)/vessel permeability factor (VPF). The peptide is used to identify the site at which an anti-VBGF antibody binds to VBGF. The antibody is used in the method of the invention, which relates to the use of an anglogenesis inhibitor. The inhibitor contains a VBGF antagonist (preferably the anti-VBGF antibody) and minocycline. The anglogenesis inhibitor can be used as a therapeutic agent against tumours. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vascular endothelial cell growth factor; vessel permeability factor; VPF; angiogenesis inhibitor; minocycline; tumour; diabetic retinopathy; intraocular angiogenic disease; aging muscular degeneration; psoriasis; rheumatoid arthritis; Kaposi's sarcoma; cancer; arteriosclerosis; VEGF.
                                                                    Thermotherapy for treatment of various cancers - involves destroying the tumor site by hot temperature and inhibiting angiogenesis effect by VEGF/VPF antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiogenesis inhibitor for treating tumors and cancers - contains vascular endothelial cell growth factor or vessel permeability factor antagonist and minocycline as active ingredient.
                                                                                                                                                                                                                                                                                                                                                                                                       54.9%; Score 73; DB 3; Length 12; 100.0%; Pred. No. 0.00015; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vascular endothelial cell growth factor peptide 61.
                                                                                                                                               Disclosure; Page 6; 8pp; Japanese.
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(TOAG ) TOA GOSEI CHEM IND LID.
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                                                                                                                                                                                                                                                                                                                            the present invention
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                                    WPI; 2000-057134/05
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inhibitor can also be used as a therapeutic agent against, intraocular angiogenic diseases such as diabetic retinopathy and aging muscular degeneration. Diseases such as rhemmatoid arthritis, psoriasis, Raposi's sarcoma, and arteriosclerosis, can also be treated using the angiogenesis
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Job time : 53 secs
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 Query Match
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                                                                                                                    March 8, 2004, 11:47:43 ; Search time 33 Seconds (without alignments) 147.167 Million cell updates/sec
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1: /cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

3: /cgn2_6/prodata/2/pubpaa/PCT_NEM_PUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/PCT_NEM_PUB.pep:*

4: /cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB.pep:*

7: /cgn2_6/prodata/2/pubpaa/USO8_NEM_PUB.pep:*

9: /cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/prodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

12: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

14: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

15: /cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

16: /cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*

16: /cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*

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16: /cgn2_6/prodata/2/pubpaa/USO0_PUBCOMB.pep:*
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-313-986-546
US-10-313-986-546
US-10-215-484-44
US-10-215-484-44
US-10-215-759-2
US-10-216-484-37
US-10-216-484-37
US-10-216-484-37
US-10-216-484-37
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US-10-216-484-37
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US-10-216-484-37
US-10-216-484-37
US-10-216-484-37
US-10-216-759-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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1 QGQHIGEMSFLQHNKCECRPKKD 23
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Maximum Match 100%
Listing first 45 summaries
                                                                                        protein search, using sw model
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Match Length
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                                                                                        OM protein
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Sequence 2203, Ap Sequence 134, App Sequence 873, App Sequence 5. Applications of the sequence 15. Applications of the sequence 15. App Sequence 516, App Sequence 516, App Sequence 116, App Sequence 140, App Sequence 140, App Sequence 243, App Sequence 243, App Sequence 243, App Sequence 243, App Sequence 243, App Sequence 135, App Sequence 137, App Sequence 140, App Sequence 137, App Sequence 140, App Sequence 137, App Sequence 140, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Sequence 137, App Se
                                                                                                                          Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 121, Appl
Sequence 1213, Ap
Sequence 1667, Appl
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APPLICANT: ACHEN, MARC
APPLICANT: ACHEN, STEVEN
APPLICANT: ACHEN, Steven
APPLICANT: CENDRON, Angela
TITLE OF INVENTION: VEGP-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION: VEGP-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION: VEGP-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
FILE REPERENCE: 1064/4855 ACHEN
CURRENT APPLICATION NUMBER: US/09/761,636A
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: US 60/204,590
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 34
SEQ ID NOS: 34
SEQ ID NOS: 34
SEQ ID NOS: 34
TANGEMENT OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO OF SECONO 
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OTHER INFORMATION: Amino acid residues Gln113-Asp153 of VEGF165
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US-09-956-508A-1
4 US-10-215-759-1
4 US-10-216-464-1
4 US-10-346-484-1
4 US-10-138-172-17
4 US-10-138-172-17
4 US-10-138-172-17
4 US-10-225-567A-1213
4 US-10-225-567A-1213
4 US-09-645-160-14
6 US-09-645-160-14
6 US-09-572-404B-2203
6 US-09-573-404B-2203
7 US-09-573-404B-2203
7 US-09-573-404B-2203
7 US-09-573-443-20
7 US-09-573-443-20
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7 US-09-573-443-20
7 US-09-573-443-20
7 US-09-573-443-20
7 US-09-573-444-46A-1440
7 US-10-26-457-243
7 US-10-26-457-243
7 US-10-286-457-243
7 US-10-286-457-243
7 US-10-286-457-257-32
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Matches 23, Conservative
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APPLICANT: Berizawa, No. US20030170817Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
TITLE OF INVENTION: Anti-Psa Antibodies
TITLE OF INVENTION: Anti-Psa Antibodies
TITLE OF INVENTION: Anti-Psa Antibodies
TITLE OF INVENTION: Anti-Psa Antibodies
TITLE OF INVENTION: Anti-Psa Antibodies
TITLE OF INVENTION: AUGUSCIP/US
CURRENT RELING DATE: 2000-26-05
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
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Pred. No. 66;
2; Mismatches 2; Indel8
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             APPLICANT: Serizawa, No. US20030103976Alufusa APPLICANT: Berizawa, No. US20030103976Alufusa APPLICANT: Haruyama, Hideyuki
APPLICANT: Haruyama, Kaori
APPLICANT: Tawaki, Ikuko
APPLICANT: Tawaki, Ikuko
APPLICANT: Tawaki, Tohru
TITIE OF INVENTION: Anti-Fras Antibodies
FILE REFRENCE: 980126C1P/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR PELING DATE: 2000-02-09
PRIOR PELING DATE: 2000-02-09
PRIOR PELING DATE: 1998-04-01
NUMBER: OF SEQ ID NOS: 165
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/10384933
Publication No. US20030170817A1
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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US-10-384-933-36
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GENERAL INFORMATION:
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LENGTH: 20
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Patent No. US20020151680A1
GENERAL INFORMATION:
APPLICANT: Alitalo et al
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
FILE REPRENCE: 28967/339778
CURRENT APPLICATION NUMBER: US/09/795,006A
CURRENT APPLICATION NUMBER: US 60/205,331
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: PATENTH VØT: 2.0
SEQ ID NO 135
LENGTH: 14
                                                                                               APPLICANT: ALILALO et al TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR TITLE OF INVENTION: ENDOTHBLIAL GROWTH FACTOR DNAS AND PROTEINS FILE REFERENCE: 28967/339778

CURRENT APPLICATION NUMBER: US/09/795,006A

CURRENT PILING DATE: 2001-02-26

PRIOR PILING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-25

NUMBER OF SEQ ID NOS: 175

SOFTWARE: PARENTIN VEY: 2.0

SEQ ID NO 136

LENGTH: 13
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US-09-795-006A-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: peptide US-09-795-006A-136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.4%; Score 79; DB 9; Length 13; 100.0%; Pred. No. 2.8e-05; tive 0; Mismatches 0; Indels
                     Sequence 136, Application US/09795006A Patent No. US20020151680A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
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Best Local Similarity
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US-09-795-006A-135
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Gaps

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Sequence 44, Application US/10384933
; Sequence 44, Application US/10384933
; Publication No. US20030170817A1
GENERAL INFORMATION:
APPLICANT: Serizawa, No. US20030170817A1ufusa
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2000-02-05
PRIOR FILING DATE: 2000-02-05
PRIOR FILING DATE: EARLIER EARLIER
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
NUMBER OF SEQ ID NOS: 165
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| Publication No. US20030059430A1
| Publication No. US20030059430A1
| Publication No. US20030059430A1
| Publication No. US20030059430A1
| TITLE OF INVENTION: IGF-BINDING PROTEIN-DERIVED PEPTIDE OR TITLE OF INVENTION: SMALL MOLECULE | FILE REFERENCE: 5149020002000
| CURRENT APPLICATION NUMBER: US/10/215,759 | CURRENT PILING DATE: 2002-08-09 | PRIOR APPLICATION NUMBER: US/60/323,267 | PRIOR APLICATION NUMBER: 06/323,267 | PRIOR PILING DATE: 2001-09-18 | SMADRE FORESEQ FOR Windows Version 4.0 | SEQ ID NO 2 | LENGTH: 20
                                                                                                                                                                                                                        24.1%; Score 32; DB 14; Length 10; 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.1%; Score 32; DB 14; Length 10; 66.7%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                       1; Mismatches
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PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 44
PRIOR FILING
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                       4; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                           Best_Local Similarity
Matches 4; Conserv
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Matches 4; Conserv
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                                                                                                                                                                              US-10-216-484-44
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TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
TITLE OF INVENTION: E9967/359778
FILE REFERENCE: 28967/359778
CURRENT APPLICATION NUMBER: U$ (09/205, 331
FRIOR APPLICATION NUMBER: U$ 60/205, 331
FRIOR FILING DATE: 2000-05-18
FRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 175
SEQ ID NO 145
LENGTH: 13
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APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
FILE REFERENCE: 200121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SEQ ID NOS: 560
SEQ ID NO 546
LENGTH: 20
                                                                                                                                                                                                                                                                                                            Score 34; DB 15; Length 20;
Pred. No. 2.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 9; Length 13;
Pred. No. 2.5e+02;
0; Mismatches 6; Indels
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Sequence 44, Application US/10216484

Publication No. US20030103976A1

SEQUENCE 41. Natural 42. No. US2003103976A1

APPLICANT: Haruyama, Hideyuki

APPLICANT: Haruyama, Hideyuki

APPLICANT: Takahashi, Tohru

APPLICANT: Takahashi, Tohru

TITLE OF INVENTION: Anti-Fas Antibodies

FILE REFERENCE: 980126CIP/HG

CURRENT APPLICATION NUMBER: US/10/216,484

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US/09/499,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 145, Application US/09795006A Patent No. US20020151680A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               25.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66./",
"hea 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Conservative
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                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-313-986-546
                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||| ::|
5 QGQHIKQLS 13
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Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                           TYPE: PRT
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Sequence 37, Application US/10384933
; Sequence 37, Application US/10384933
; Publication No. US20030170817A1
; Publication No. US20030170817A1
; GENERAL INFORMATION:
APPLICANT: Haruyama, Hideynki
APPLICANT: Tamahara, Kaori
APPLICANT: Takahari, Tohru
ITILE OF INVENTION: Anti-Fas Antibodies
TITLE OF INVENTION: Anti-Fas Antibodies
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CTF/HG
CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: EARLIER PLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-04-01
PRIOR PILLING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
LEGGTH: 20

LEGGTH: 20

LEGGTH: 20

LEGGTH: 20

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; Sequence 7, Application US/10215759
; Sequence 7, Application No. USCO30059430A1
; Publication No. USCO30059430A1
; GENERAL INFORMATION:
APPLICANT: Mascarenhas, Desmond
TITLE OF INVENTION: INFA INDING PROTEIN-DERIVED PEPTIDE OR
TITLE OF INVENTION: SEAALL MOLECULE
; TITLE OF INVENTION: SEAALL MOLECULE
; TITLE OF INVENTION: SAALL MOLECULE
; TILLE OF INVENTION NUMBER: US/10/215,759
CURRENT FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 22
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                                                                                                                                                                                                                              Query Match 24.1%; Score 32; DB 14; Length 20; Best Local Similarity 50.0%; Pred. No. 5.3e+02; Matches 5; Conservative 2; Mismatches 3; Indels Matches
CHER INCRMATION: Synthetic construct prature:

| FRATURE:
| NAME(RET: PEPTIDE:
| LOCATION: (1) ... (20)
| FRATURE:
| NAME(RET: METAL:
| LOCATION: (8) ... (19)
| US-10-264-672-2
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ORGANISM: Artificial Sequence
FRATURE:
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US-10-384-933-37
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US-10-384-933-37
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; Sequence 2, Application US/10264672
; Sequence 2, Application No. US20030161829A1
; Publication No. US20030161829A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENHAS, Desmond
; TITLE OF INVENTION: IGF-BINDING PROTEIN-DERIVED PEPTIDE OR
; TITLE OF INVENTION: SMALL MOLECULE
; FILE REFERENCE: 51492000220
; CURRENT APPLICATION NUMBER: US/10/264,672
CURRENT FILING DATE: 2003-03-13
; PRIOR FILING DATE: 2003-09-09
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 36
; SOFTRARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LEAGTH: 20
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                                                                                                                                                                                                                              Query Match 24.1%; Score 32; DB 14; Length 20; Best Local Similarity 50.0%; Pred. No. 5.3e+02; Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-216-484-37

US-10-216-484-37

Sequence 37, Application US/10216484

PUblication No. US20030103976A1

GENERAL INFORMATION:

APPLICANT: Baruyama, No. US20030103976Alufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Takahashi, Tohru
TITLE OP INVENTION: Anti:Fas Antibodies
FILE REPERRENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216, 484
CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US/09/499, 662

PRIOR APPLICATION NUMBER: US/09/499, 662

PRIOR APLICATION NUMBER: US/09/499, 662

PRIOR APLICATION NUMBER: US/09/499, 662

PRIOR FILING DATE: 2000-02-09

PRIOR APPLICATION NUMBER: US/09/499, 662

PRIOR PILING DATE: 1998-04-01

NUMBER OF SEQ ID NOS: 165

SEQ ID NO 37

LENGUETH: 20
          OTHER INFORMATION: Synthetic construct
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                        3 YKKKQCRPSK 12
                                                                                                                                                                                                                                                                                                                                                  13 HNKCECRPKK 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-216-484-37
                                                                                  LOCATION: (1) ... (20) FEATURE: NAME/KEY: METAL LOCATION: (8) ... (19)
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1 KCRCKP 6
                                         FEATURE:
NAME/KEY: PEPTIDE
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                                                                                                                                                                                          US-10-215-759-2
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LOCATEN 101...(22)
OTHER INPORMATION: Capable of directing cellular internalization of
OTHER INPORMATION: unrelated proteins.
                       FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(22)
COTHER INFORMATION: Capable of directing cellular internalization of OTHER INFORMATION: Capable of directing cellular internalization of OTHER INFORMATION: unrelated proteins.
FRATURE:
NAME/KEX: METAL
LOCATION: (10)...(21)
COTHER INFORMATION: (20)
US-10-215-759-7
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; Sequence 7, Application US/10264672
; Sequence 7, Application Wo. US2030161829A1
; GENERAL INFORMATION:
; APPLICANT: MASCARENIAS, Desmond
; TITLE OF INVENTION: IGF-BINDING PROTEIN-DERIVED PEPTIDE OR
; TITLE OF INVENTION: SMALL MOLECULE
; FILLE REFRENCE: 51492000220
; CURRENT APPLICATION NUMBER: US/10/264,672
CURRENT PILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: US 10/215,759
PRIOR PILING DATE: 2000-09-18
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 36
SOFTWARE: FASTERO for Windows Version 4.0
; SEQ ID NOS: 36
; SEQ ID NOS: 37
ILENGTH: 22
: TYPE: PRT
: ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.1%; Score 32; DB 14; Length 22; Best Local Similarity 50.0%; Pred. No. 5.9e+02; Matches 5; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                               Score 32; DB 14; Length 22;
Pred. No. 5.9e+02;
                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: METAL
LOCATION: (10)...(21)
COTHER INFORMATION: Selectively binds zinc and nickel
US-10-264-672-7
                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic construct FRATURE:
OTHER INFORMATION: Synthetic construct
                                                                                                                                                                                                                                                                    Query Match 24.1%;
Best Local Similarity 50.0%;
Matches 5; Conservative 2
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5 YKKKQCRPSK 14
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-264-672-7
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Search completed: March 8, 2004, 11:53:02 Job time : 33 secs